

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 15, 2005, 12:29:05 ; Search time 129 Seconds
(without alignments)
9576.067 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 2848
Sequence: 1 ctcgagattacccttacag.....gaaataaattatctcgtgcc 1597

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlp
-Q=/cgn2_1/USPTO.spool_p/US10775649/runat.14062005.141110.20646/app.query.fasta.1.1735
-DB=A Geneseq.16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10775649 @CGN 1.154 @runat.14062005.141110.20646 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSFPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -TIMEOUTS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq.16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1802	63.3	343	5 ABB08277	Abb08277 Murine mu
2	1671	58.7	351	5 ABB81134	Abb81134 Rat MURF1
3	1619.5	56.9	370	4 AAM00918	Aam00918 Human bon
4	1613	56.6	353	4 ABB50234	Abb50234 Human tra
5	1613	56.6	353	5 ABB93804	Abb93804 Human bon
6	1613	56.6	353	6 ADA55293	Ada55293 Human pro
7	1613	56.6	353	7 ADE61549	Ade61549 Human pro
8	1613	56.6	353	7 ADE61546	Ade61546 Human pro
9	1612.5	56.6	366	4 AAU15855	Aau15855 Human nov
10	1612.5	56.6	366	6 ABU54924	Abu54924 Human nov

11	1583.5	55.6	366	4 AAU25438	Aau25438 Human mdd
12	1562	54.8	340	5 ABB81135	Abb81135 Human MUR
13	1378	48.4	302	4 AAM00998	Aam00998 Human bon
14	1126.5	39.6	452	6 AAE32110	Aae32110 Human cyt
15	1126.5	39.6	452	7 ADB64249	Adb64249 Human pro
16	1126.5	39.6	548	7 ADB64489	Adb64489 Human pro
17	1115	39.2	412	7 ADC31770	Adc31770 Human nov
18	1114.5	39.1	545	5 ABB08276	Abb08276 Murine mu
19	1110	39.0	366	5 ABB08275	Abb08275 Murine mu
20	1107	38.9	358	4 AAG63832	Aag63832 Amino aci
21	1107	38.9	358	4 AAG93278	Aag93278 Human pro
22	1107	38.9	358	7 ADC31154	Adc31154 Human nov
23	1103.5	38.7	396	3 AAB21048	Aab21048 Human nuc
24	1073	37.7	201	5 ABB81142	Abb81142 Rat MURF1
25	1070	37.6	400	5 ABB81144	Abb81144 Human MUR
26	1015	35.6	289	5 ABB81145	Abb81145 Human MUR
27	985	34.6	326	5 ABB83475	Abb83475 Human cyt
28	979.5	34.4	414	4 AAU15868	Aau15868 Human nov
29	979.5	34.4	414	6 ABU54937	Abu54937 Human tra
30	886	31.1	254	4 AAB61322	Aab61322 Human tra
31	846	29.7	602	8 ADP22642	Adp22642 Sea-squir
32	771.5	26.4	218	4 AAM00805	Aam00805 Human bon
33	764	26.8	143	3 AAB41076	Aab41076 Human ORF
34	764	26.8	143	5 ABP34078	Abp34078 Human int
35	676.5	23.8	181	7 ADC33320	Adc33320 Human nov
36	652.5	22.9	184	4 AAU16327	Aau16327 Human nov
37	652.5	22.9	184	6 ABU55396	Abu55396 Human nov
38	504	17.7	122	4 AAU16316	Aau16316 Human nov
39	504	17.7	122	6 ABU55385	Abu55385 Human nov
40	455	16.0	524	8 ADR09855	Adr09855 Human pro
41	436.5	15.3	736	7 ADM04867	Adm04867 Human pro
42	432.5	15.2	552	7 ADJ70562	Adj70562 Human hea
43	432.5	15.2	667	8 ADQ21458	Adq21458 Human sof
44	418.5	14.7	716	7 ADD01211	Add01211 Human nuc
45	406.5	14.3	744	4 ABG18061	Abg18061 Novel hum

ALIGNMENTS

RESULT 1

ABB08277
ID ABB08277 standard; protein; 343 AA.

XX ABB08277;
XX
XX 15-JUL-2002 (first entry)
XX
XX Murine muscle ring finger protein 3 (MURF-3).
XX
XX Muscle ring finger; MURF-3; mouse; cardiant; microtubule;
XX intermediate filament; striated muscle; cardiac hypertrophy;
XX heart disease.
XX
XX Mus musculus.
XX
XX WO200206318-A2.
XX
XX 24-JAN-2002.
XX
XX 18-JUL-2001; 2001WO-US022896.
XX
XX 18-JUL-2000; 2000US-0219020P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Olson EN, Spencer JA;
XX
XX WPI; 2002-241506/29.
XX N-PSDB; ABA99063.
XX
XX Novel muscle ring finger protein useful for drug screening, and for
XX diagnosing and treating diseases, particularly cardiomyopathies.
XX

PS Claim 3; Fig 10; 134pp; English.

XX The sequence represents murine muscle ring finger protein 3 (MURF-3). The
 CC invention relates to a purified muscle ring finger (MURF) protein,
 CC selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the
 CC invention are involved in microtubule and intermediate filament
 CC stabilisation of striated muscle cells and have cardiant activity. The
 CC MURF proteins are useful for screening a candidate substance for MURF
 CC protein-binding activity, in a cell, cell-free system or in vivo, and its
 CC effect on interaction of MURF with microtubules, homodimerisation of
 CC MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction
 CC of MURF with intermediate filaments, e.g. desmin, vimentin and
 CC cyokeratin, and heterodimerisation of MURF. The screened compounds are
 CC useful for treating and preventing cardiac hypertrophy and heart
 CC diseases. MURF proteins are useful as antigens to immunise animals for
 CC the production of antibodies

XX SQ Sequence 343 AA;

Alignment Scores:
 Pred. No.: 7.39e-147 Length: 343
 Score: 1802.00 Matches: 343
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 63.27% Indels: 0
 DB: 5 Gaps: 0

US-10-775-649-5 (1-1597) x ABB08277 (1-343)

QY 299 ATGGATTATAAATCTAGCTGATTCCTGATGGAACGCTATGGAACCTGGAGAACGACG 358
 DB 1 MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluGln 20
 QY 359 CTGATCTGCCCATCTCCCTGGAGATGTTTACCAAGCCTGTGTCATCTGCCCTGCCAA 418
 DB 21 LeuileCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40
 QY 419 CACAACTCTGCCGGAAGTGTGCCAACGACATCTCCAGGCTCGAATCCCTACTCGACC 478
 DB 41 HisAsnLeuCyshgysCysAlaAsnAspIlePheGlnAlaAlaAsnProIlyrPthr 60
 QY 479 AACCCGGTGGCTCAGTGTCCATGTCTGGAGGTGCTTCCGTTGCCCTCGTCGCCCAT 538
 DB 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysAghis 80
 QY 539 GAAGTCATATGACCGGACCGGGTGTACGGCTCGAGGAACTGCTGTGGAAAC 598
 DB 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
 QY 599 ATCATTGACATCTACAGCAGGAGTGTCCAGTCGGCCCTCGAGAAAGCAGCCACCG 658
 DB 101 IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
 QY 659 ATGTCAAGAAACACCAAGACGAGAATCAACATCTACTGTCTCAGTGTGAGGTGCTT 718
 DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
 QY 719 ACTGTCTCTTGTGCAAGTGTGTGGGCTCACCAGCCCTGTCAGGTTGCCCTTTGCAA 778
 DB 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
 QY 779 AGCATCTTCAAGACAGAAAGCTGAGCTGAGTGAAGTAACTGCATCTCCATCTGTTGGGGGG 838
 DB 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
 QY 839 AACGACCGAGTCAGACGATCATCTCTCAGCTGAGGACTCGTCAGAGTGACCAAGAG 898
 DB 181 AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
 QY 899 ATAGCCACGAGTGAAGGAGGCTGAGTCAGAGTTTGACACCTCTACGCCATCTG 958
 DB 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220

QY 959 GATGAGAAGAGAGAGAGCTGCTGACGCGATCACGACGAGCAGGAGAGCTGGGC 1018
 DB 221 AspGluLysLysSerGluLeuLeuGlnAglIleThrGlnGlnGlnGluLysLeuGly 240
 QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG 1078
 DB 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
 QY 1079 GAGACCCCATCCAGTCCCTGATGAGCCGCGAGGGCTACCTCTCTCAAGTGCACAG 1138
 DB 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuSerSerAlaLys 280
 QY 1139 CAGCTCATCAAGAGCATTCTAGAACGCTCCAAAGGCTGCAGCTGGGGAAGACAGACAA 1198
 DB 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
 QY 1199 GGCTTTGAGAACATGGACTACTTTACTTGGACTTAGAACACATAGCAGGCTTGGAG 1258
 DB 301 GlyPheGluAsnMetAspTyrPheThrLeuAspLeuGluHisIleAlaGluAlaLeuArg 320
 QY 1259 GCATTGACTTTGGGACAGCTAAAGATGCTGATGTACATGTTGACCTTTGAAAGCAG 1318
 DB 321 AlaIleAspPheGlyThrGlyLysGlyCysAspValThrCysLeuThrPheGluArgGln 340
 QY 1319 CGTTCCTCT 1327
 DB 341 ArgSerSer 343
 RESULT 2
 ABB81134
 ID ABB81134 standard; protein; 351 AA.
 XX AC ABB81134;
 XX DT 05-NOV-2002 (first entry)
 XX DE Rat MURF1 protein.
 XX KW Muscle atrophy protein; MURF1; MURF3; MAFB3; atrophy; neuroprotective;
 XX OS Rattus sp.
 XX PN WO200261046-A2.
 XX PD 08-AUG-2002.
 XX PF 30-JAN-2002; 2002WO-US002811.
 XX PR 30-JAN-2001; 2001US-0264926P.
 XX PR 10-AUG-2001; 2001US-0311697P.
 XX PR 22-OCT-2001; 2001US-0338742P.
 XX PA (REGE-) REGENERON PHARM INC.
 XX PI Glass DJ, Bodine SC;
 XX DR WPI; 2002-608513/65.
 XX DR N-PSDB; ABQ79506.
 PT Isolated nucleic acid molecules encoding muscle atrophy proteins, e.g.
 PT MURF1, MURF3 or MAFB3, useful for treating muscle atrophy and other
 PT related disorders, e.g. Guillian-Barre syndrome, peripheral neuropathy,
 PT and nerve damage.
 XX Claim 1; Fig 7; 104pp; English.
 CC The invention relates to isolated nucleic acid molecules encoding muscle
 CC atrophy proteins MURF1, MURF3, or MAFB3. The proteins can be expressed by
 CC standard recombinant methodology. The nucleic acid molecules and
 CC polypeptides are useful for treating muscle atrophy or detecting atrophy,
 CC and for treating related diseases/disorders, e.g. Guillian-Barre
 CC syndrome, peripheral neuropathy, or nerve damage caused by environmental

CC toxins or drugs. The MURF1, MURF3 and MAFB antagonists, and the
CC antagonists of their pathways are useful for inhibiting atrophy, inducing
CC hypertrophy, decreasing ubiquitination, interfering with the ubiquitin
CC pathway, or modulating MURF1, MURF3 or MAFB expression or activity. The
CC nucleotide sequences are useful for diagnostic and genetic testing. The
CC present sequence represents a rat MURF1 protein
XX
SQ Sequence 351 AA;

Alignment Scores:
Pred. No.: 1,67e-135 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.18% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 5 Gaps: 0

US-10-775-649-5 (1-1597) x ABB81134 (1-351)

QY 299 ATGGATTATAATCTAGCTGATCTCTGATGAAACGCTATGAGAACCTGGAGAGCAG 358
Db 1 MetAspTyrLysSerGlyLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTGCTGGAGATGTTACCAAGCCTGTGTCATCTGCCCTGCCAA 418
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACCTCTGCCGAAGTGTCCCAACGACATCTTCCAGGCTGCCAATCCCTACTGACCC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCCGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCGTGGCCGCAT 538
Db 61 AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGGACCGGACGGGTGTACGGCTGCAGAGGAACCTGCTGTGGAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGAGTGTCTCAGTCCGGCCCTGCAGAAAGGACGACCCG 658
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTCAAGGACACAGAACGAGAGTCAACATCTACTGTCTCAGTGTGAGTGTGCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTGTGCAAGGTGTTTGGGCTCACCAGGCTGTGAGTGTGCCCTTTGCCAA 778
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACAGAGACTGAGTGAAGTAACTGCATCTCCATGCTGTGGCGGG 838
Db 161 SerIlePheGlnGlyValLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTCAGAGTGCACCAAGAG 898
Db 181 AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 ATAGCCACCGAGTGCAGAGGAGTGTGAGTGAAGTTTGACACCTCTACGCCATCTGTG 958
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
QY 959 GATGAGAAGACGAGTGTGTCAGCGGATCAGCAGGACGAGGAGGAGTGTGGC 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGlnGluLysLeuAsp 240
QY 1019 TTCATCGAGGCTCTGATCTCTCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATCAGTCTCTGATGAGCCGAGGGGTACCTTCTCTCAAGTCCCAAG 1138

Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAAGAGCATTGTAGAAGCCCTCAAGGCTCCAGCTGGGAAGACAGACAA 1198
Db 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCCTTTGAGAACATGGACTACTTCTGACTTAGAACACATAGACAGGCGCTTGAGG 1258
Db 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaIleAspPheGlyThr 326
RESULT 3
AAM00918
ID AAM00918 standard; protein; 370 AA.
XX
AC AAM00918;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human bone marrow protein, SEQ ID NO: 394.
XX
KW Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
KW immunosuppressive; gene therapy; cytokine cell proliferation;
KW cell differentiation modulator; immune disorder; infection; cancer;
KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
XX
OS Homo sapiens.
XX
PN WO200153453-A2.
XX
PD 26-JUL-2001.
XX
PF 23-DEC-2000; 2000WO-US034960.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 30-NOV-2000; 2000US-0250583p.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
PI Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Drmanac RT;
XX
XX WPI; 2001-488707/53.
DR N-PSDB; AAH90037.
XX
PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful for
PT treating e.g. cancer and immune deficiency disorders.
XX
PS Claim 10; Page 481-482; 648pp; English.
XX
CC The present sequence is one of 251 novel human polypeptides encoded by a
CC bone marrow-expressed polynucleotide. The polynucleotide and the
CC polypeptide encoded by it are useful in the treatment of various immune
CC deficiencies and disorders. The deficiencies and disorders may be
CC genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC infection, or may result from an autoimmune disorder, a coagulation
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC suppression of an inflammatory response or treatment of a nervous system
CC disorder such as Alzheimer's disease. Detection of the presence or
CC increased expression of the polynucleotide or the protein it encodes is
CC useful for the diagnosis and/or prognosis of one or more types of cancer.

CC The polynucleotide and polypeptide can be used as nutritional sources or
XX supplements and in the screening of chemical compounds as potential drugs
SQ Sequence 370 AA;

Alignment Scores:
Pred. No.: 4.95e-131 Length: 370
Score: 1619.50 Matches: 309
Percent Similarity: 94.48% Conservative: 16
Best Local Similarity: 89.83% Mismatches: 14
Query Match: 56.86% Indels: 5
DB: 4 Gaps: 1

US-10-775-649-5 (1-1597) x AAM00918 (1-370)

QY	245	AGACAAGACTTGGTGTGACGAGGTGGGCAACAGACAGTCGCATTTCAAGCAATATGGAT	304
DB	1	ArgArgGlnLeuGlyValAlaLeuIlePro- - - - -SerHisArgMetAsp	15
QY	305	TATAAATCTAGCCTGATTCCTGATGAACCGTATGGAGAACCTGGAGAGCAGCTGATC	364
DB	16	TyLysSerSerLeuLeuGlnAspGlyAsnProMetGluAsnLeuGluysGlnLeuIle	35
QY	365	TGCCCCATCTGCTGGAGATGTTTCAACAGCCTGTGTCATCTCCCTGCCCTGCCAACAC	424
DB	36	CysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGlnHisAsn	55
QY	425	CTTGCGGAGTGTCCCAACGACATCTCCAGGCTGCGATCCCTACTGGACCAACCGC	484
DB	56	LeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThrSerArg	75
QY	485	GGTGGCTCAGTGTCCATGTCTGAGAGTGGTTCCTGTCGCCCTGCGCGCATGAAGTG	544
DB	76	GlySerSerValSerMetSerGlyLysArgPheArgCysProThrCysArgHisGluVal	95
QY	545	ATCATGACCGGCACGGGGTGTACGCCCTGTCAGAGGAACCTGCTGTGGAAACATCAT	604
DB	96	IleMetAspArgHisGlyValTyGlyLeuGlnArgAsnLeuValGluAsnIleIle	115
QY	605	GACATCTACAGCAGGAGTCTCCAGTCCGCCCTGCAGAAAGCCAGCCCGATGTC	664
DB	116	AspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisProMetCys	135
QY	665	AAGCAACACGAACAGACAGAGATCAACATCTACTGTCTCAGGTGAGGTGCTACTTGC	724
DB	136	LysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValProThrCys	155
QY	725	TCCTTGTCAAGGTGTTTGGGGCTCACAGCGCTGTGAGGTGCCCTTTGCAAGCATC	784
DB	156	SerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGlnSerVal	175
QY	785	TTCACAGGACAGAGACTGAGTGAATCTCCATCTCCATGCTGGTGGGGGACGAC	844
DB	176	PheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGlyAsnAsp	195
QY	845	CGAGTGCACAGCATCTCTCAGCTGGAGGACTCGTCGACAGTGCACCAAGAGAGATAGC	904
DB	196	ArgValGlnThrIleLeuThrGlnLeuGluAspSerArgValThrLysGluAsnSer	215
QY	905	CACAGGTGAAGAGAGTGTAGTCTAGAGTTTGACACCTCTACCCCTCTCGGTGATAG	964
DB	216	HisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeuAspGlu	235
QY	965	AGAAGACGAGCTGTGACGGATCAGCGAGGACGAGGAGAGCTGGGCTCATC	1024
DB	236	LysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnLysLysLeuSerPheIle	255
QY	1025	GAGGCTCTCATCTCCAGTACAGGACGAGCTGGAAGTCCACCAAGCTTTGGAGAC	1084
DB	256	GluAlaLeuIleGlnGlnTyrGlnGlnGlnLeuAspLysSerThrLysLeuValGluThr	275
QY	1085	GCCATCCAGTCCCTGATAGCCCGGAGGGGTACCTTCTCTCAAGTCCAGCAGCTC	1144

Db	276	AlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLysGlnLeu	295
QY	1145	ATCAAGAGCATTTGTAGAACCTCCAGGGCTCCAGCTGGGAGACAGACAGGCTTT	1204
Db	296	IleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGlnGlyPhe	315
QY	1205	GAGAACATGGACTACTTTTACTCTGGACTTAGAACACATAGCAGAGCCCTTGAGGGCATT	1264
Db	316	GluAsnMetAspPhePheThrLeuAspLeuGluHisIleAlaAspAlaLeuArgAlaIle	335
QY	1265	GACTTTGGGACA	1276
Db	336	AspPheGlyThr	339

RESULT 4
ABB50234
ID ABB50234 standard; protein; 353 AA.
XX
AC ABB50234;
XX
DT 05-FEB-2002 (first entry)
XX
DE Human transcription factor TRFX-85.
XX
KW Human; transcription factor; TRFX; cell proliferative disease;
KW autoimmune disease; inflammation; neurological disease;
KW developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;
KW neuroprotective; antiinflammatory; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200172777-A2.
XX
PD 04-OCT-2001.
XX
PF 13-MAR-2001; 2001WO-US008117.
XX
PR 13-MAR-2000; 2000US-018986P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Hillman JL, Baughn MR, Yue H, Lal P, Lu DAM, Patterson C;
PI Azimzai Y, Bandman O, Tang YT, Mathur P, Shah P, Au-Young J;
PI Reddy R;
XX
DR WPI; 2001-570896/64.
DR N-PSDB; ABA83058.
XX
PT Novel transcription factor polypeptides, used to treat diseases
PT associated with altered activity and expression of TRFX, and to screen
PT for agents capable of modulating its activity.
XX
PS Claim 1; Page 227-228; 327pp; English.
XX
CC The present sequence is the protein sequence for a human transcription
CC factor. The transcription factor and its coding sequence are useful in
CC the diagnosis, treatment and prevention of diseases associated with
CC altered expression of the transcription factor e.g. cell proliferative,
CC autoimmune/inflammatory, neurological and developmental disorders. A
CC number of specific disorders/diseases are given in the specification,
CC including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS,
CC allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic
CC dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout,
CC Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis, psoriasis,
CC rheumatoid arthritis, systemic lupus erythematosus, ulcerative
CC colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, stroke, and viral, bacterial, fungal and protozoal infections
XX
SQ Sequence 353 AA;

Alignment Scores:
Pred. No.: 1.77e-130 Length: 353
Score: 1613.00 Matches: 305

Percent Similarity:	97.55%	Conservative:	13
Best Local Similarity:	93.56%	Mismatches:	8
Query Match:	56.64%	Indels:	0
DB:	4	Gaps:	0

US-10-775-649-5 (1-1597) x ABB50234 (1-353)

Qy	299	ATGANTTAATAATCTAGCCTGATTCCTGATGTGAAGAACTGATCGAAGCACTGAGAAAGCAAG	358
Db	1	MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln	20
Qy	359	CTGATCTGCCCATCTGCCTGGAGATGTTTACCAAGCCCTGCTGTCATCTCGCCCTGCCAA	418
Db	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40
Qy	419	CACAACTCTGCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGAGCC	478
Db	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr	60
Qy	479	AACCGCGTGGCTCAGTCTCCATGTCCTGAGGTGCTTTCCGTCCTGCTGCTGCGCCCAT	538
Db	61	SerArgGlySerSerValSerMetSerGlyIleArgPheArgCysProThrCysArgHis	80
Qy	539	GAAGTGATCATCGGACCGGCACGGGTGTACGGCCTGCAGAGAACTCTGTGTGGAAAC	598
Db	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsn	100
Qy	599	ATCATTGACATCTACAGCAGAGAGTCTCCAGTCCGCCCTCGAGAAAGCAGCCACCCG	658
Db	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120
Qy	659	ATGTCAAGGAACACGAACAGAGAAAGATCAACATCTACTGTCTCACGTGTGAGTGCCT	718
Db	121	MetCysLysGluHisIleGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140
Qy	719	ACTTGTCTCTGTGCAGAGTGTGGGCTCACAGGCTGTGAGGTTGCCCTTTGGCAA	778
Db	141	ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln	160
Qy	779	AGCATCTTCCAAAGGACAGAAGACTCAGCTGAGTAACTGTCATCTCCATGCTGTGGCGGG	838
Db	161	SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly	180
Qy	839	AACGACCGAGTGCAGACCATCTCTCAGCTGGAGGACTCTGTGCAGAGTGCACCAAGAG	898
Db	181	AsnAspArgValGlnThrIleIleThrGlnLeuGluAspSerArgArgValThrLysGlu	200
Qy	899	ATAGCCACCAAGTCAAGGAGAGCTGAGTCAGAGTTTGACACCTCTACGCCCATCTG	958
Db	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220
Qy	959	GATGAGAAAGAGCGCAGCTGTCTGCAGCCGATCACGCGAGGAGGAGAGAGCTGGGC	101
Db	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnLysLysLeuSer	240
Qy	1019	TTTCATCGAGGCTCTGATCTCCAGTACAGGAGAGCTGGAAGAAGTCCACCAAGCTTGTG	1079
Db	241	PheIleGluAlaLeuIleGlnGlnTyrGlnGluGlnLeuAspLysSerThrLysLeuVal	260
Qy	1079	GAGACCGCATCCAGTCCCTGTGATGAGCCCGGAGGGCTACCTTCCTCTCAAGTGCCAAG	113
Db	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys	280
Qy	1139	CAGCTCATCAAGACATGTAGAAGCCTCCAAAGGCTGCCAGCTGGGGAGACAGACAA	119
Db	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300
Qy	1199	GGCTTTGACATCGACTACTTTACTCTGGACTTAGACACATACGAGCGCTTGAG	125
Db	301	GlyPheGluAsnWeAspPhePheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg	320
Qy	1259	GCCATTGACTTTGGGACA	1276

Db 321 AlaIleAspPheGlyThr 326

RESULT 5
ABG93804
ID ABG93804 standard; protein; 353 AA.
XX
AC ABG93804;

XX	27-NOV-2002 (first entry)
DT	
XX	Human bone remodelling protein #2.
DE	
XX	Bone remodelling; osteoporosis; human.
XX	
KW	
XX	Homo sapiens.
OS	

XX US6426186-B1.
PN
XX
PD 30-JUL-2002.

XX	18-JAN-2000; 2000US-00484970.
PF	
XX	18-JAN-2000; 2000US-00484970.
PR	

XX (INCY-) INCYTE GENOMICS INC.
PA Jones KA, Volkmuth W, Walke
XX
PI

WPI; 2002-673014/72.
N-PSDB; ABS70380.

PT to be involved in bone remodeling
PT for the diagnosis of bone remodeling disorders.

PS Example 5; Col 401-403; 206pp
XX
CC The invention relates to a co

CC expressed with genes known to
CC osteoporosis. The invention i
CC bone remodelling or osteopor

XX SQ Sequence 353 AA;

Pred. No.:	1.77e-130
Score:	1613.00
Percent Similarity:	97.55%
Best Local Similarity:	97.55%

```
Query Match: 56.64%
DB: 5
IIS-10-775-649-5 (1-1597) x ABG9380
```

QY 299 ATGATTATAAATCTAGCCT
|||
Db 1 Met Asp Tyr Lys Ser Ser Le

QY 359 CTGATCTGCCCATCTGCCT
|||
pb 21 LeuIleCysProIleCysLe

QY
Db

419 CACAACCTCTGCCGGAAGTGT
|||||
41 HisAsnLeuCysArqLysCy

QY	479	AACCGCGGTGGCTCAGTGTCT
		:::
Db	61	SerArgGlySerSerValSer

Db 321 AlaIleAspPheGlyThr 326

RESULT 5
ABG93804
ID ABG93804 standard; protein; 353 AA.

AC ABG93804;
XX
DT 27-NOV-2002 (first entry)

DE Human bone remodelling protein #2.
XX
KW Bone remodelling; osteoporosis; human.
....

OS Homo sapiens.
XX
PN US6426186-B1.
???

PD 30-JUL-2002.
XX
PF 18-JAN-2000; 2000US-00484970.
vv

PR 18-JAN-2000; 2000US-00484970.
XX
XX
PA (INCY-) INCYTE GENOMICS INC.
VV

PI Jones KA, Volkmut W, Walker MG;
XX
DR WPI; 2002-673014/72.
DP N-PSDB: ABS70380

A combination of polynucleotides which are co-expressed to be involved in bone remodeling and osteoporosis are for the diagnosis of bone remodeling and osteoporosis.

FI disorders.
XX
PS Example 5; Col 401-403; 206pp; English.
XX

the invention relates to a combination comprising a substantially purified and isolated polynucleotide expressed with genes known to be involved in bone resorption. The invention is used to diagnose disorders of bone metabolism, such as osteoporosis.

CC some remodelling of cytoskeleton, membrane associated
CC remodelling proteins of the invention
XX
SQ Sequence 353 AA;

Alignment Scores:		
Pred. No.:	1.77e-130	Length: 353
Score:	1613.00	Matches: 305

```
Best Local Similarity: 93.56%
Query Match: 56.64%
DB: 5
Mismatches: 8
Indels: 0
Gaps: 0
```

US-10-775-649-5 (1-1597) x ABG93804 (1-353)

QY 299 ATGGATTATAAATCTAGCCTGATTCCTGATGGAAACGCTATGG

Db	1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGt
QY	359 CTGATCTGCCCATCTGCCTGGAGATGTTTACCAAGCCTGTGGG

Db	21	LeuIleCysProIleCysLeuGluMetPheThrLysProVal
Qy	419	CACAACCTCTGCCCGGAAGTGTGCCAACGCATCTTTCCAGGCTG

Qy 479 AACCGCGTGGCTCAGTGTCATGCTGGAGGTCGTTTCGGTTT
... |||||
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAla

```

Db  SerArgGlySerSerValSerMetSerGlyGlyArgGlyneArg
61 SerArgGlySerSerValSerMetSerGlyGlyArgGlyneArg

```

QY 539 GAAGTATCATGACCGGACGGGGTGTACGGCTCGACAGGAACTGTGTGGTGGAAAC 598
 Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
 QY 599 ATCATTGACATCTACAGCAGAGTGTCTCAGTCGGCCCTCGAGAAAGCAGCCACCG 658
 Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
 QY 659 ATGTGCAAGGAACACCAAGCAGAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCCT 718
 Db 121 MetCysLysGlnHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
 QY 719 ACTTGCTCTTGTCAAGGTGTTTGGGGCTCACAGCGCTGTGAGGTGCCCCCTTGGCAA 778
 Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
 QY 779 AGCATCTTCAGGACAGAGACTGAGTGAATCTGATCTCCATCTCCATCTGTGTGGCGGG 838
 Db 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
 QY 839 AAGCAGCGAGTGCAGAGATCTCTCTCAGCTGGAGGACTCGTCAGAGTGCACAGGAG 898
 Db 181 AsnAspArgValGlnThrIleIleThrGlnLeuGluAspSerArgValThrLysGlu 200
 QY 899 AATAGCCACCGAGTGAAGGAGGAGCTGAGTCAAGATTTTCACACCTCTACGCGCATCTG 958
 Db 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220
 QY 959 GATGAGAAGAGCAGCTGTCTGACGGGATCACGACGAGCAGGAGAGCTGGGC 1018
 Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnLysLysLeuSer 240
 QY 1019 TTCATCGAGCTCTGATCTCTCCAGTACAGGAGCAGCTCGAAAGTCCACCAAGCTGTG 1078
 Db 241 PheIleGluAlaLeuIleGlnIleGlnIleGlnIleGlnLysSerThrLysLeuVal 260
 QY 1079 GAGACCGCCATCCAGTCCCTGGATGAGCCCGAGGGGCTACCTTCTCAAGTGCACAG 1138
 Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLeuLeuThrAlaLys 280
 QY 1139 CAGCTCATCAGAGCATTTGTAGAGCCTCCAGGGCTGCGAGTGGGGAGACAGAGCAA 1198
 Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
 QY 1199 GGCTTTGAGAACATGACTACTTTACTCTGGACTTAGAACACATACAGAGCCTTGAGG 1258
 Db 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
 QY 1259 GCCATTGACTTTGGGACA 1276
 Db 321 AlaIleAspPheGlyThr 326
 RESULT 6
 ADA55293
 ID ADA55293 standard; protein; 353 AA.
 XX
 AC
 AC ADA55293;
 XX
 DT 20-NOV-2003 (first entry)
 DE
 DE Human protein, SEQ ID 2861.
 XX
 KW Cytotoxic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX
 OS Homo sapiens.
 OS
 PN EP1293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.

XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Naganari K, Masuho Y;
 XX
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA53654.
 XX
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 14; SEQ ID NO 2861; 205pp; English.
 XX
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 XX
 SQ Sequence 353 AA;
 Alignment Scores:
 Pred. No.: 1,77e-130 Length: 353
 Score: 1613.00 Matches: 305
 Percent Similarity: 97.55% Conservative: 13
 Best Local Similarity: 93.56% Mismatches: 8
 Query Match: 56.64% Indels: 0
 DB: Gaps: 6
 US-10-775-649-5 (1-1597) x ADA55293 (1-353)
 QY 299 ATGGATTATTAATCTAGCCTGATTCCTGATGAAACGCTATCGAGAACCTGGAGAGCAG 358
 Db 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
 QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCTATCTCTGCTGCCCAA 418
 Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
 QY 419 CACACCTCTCGCGGAGTGTCCCAACGACATCTCCAGGCTCGGAATCCCTACTCGACC 478
 Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
 QY 479 AACCGGTGGCTCAGTGTCCATGTCTGAGGTCTGTTTCCGTTGCCCTCGCGCCCAT 538
 Db 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
 QY 539 GAAGTGATCATGACCGGACCGGGGTGTACGGCTGTACGGAGAACCTGTGTGGTGGAAAC 598
 Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
 QY 599 ATCATTGACATCTACAGCAGAGTGTCTCAGTGGCCCTCGAGAAAGCAGCCACCG 658
 Db 101 IleIleAspIleTyrLysGlnLysCysSerSerArgProLeuGlnLysGlySerHisPro 120
 QY 659 ATGTGCAAGGACAGAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCCT 718
 Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
 QY 719 ACTTGCTCTTGTCAAGGTGTTTGGGGCTCACAGCGCTGTGAGGTGCCCCCTTGGCAA 778
 Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
 QY 779 AGCATCTTCAGGACAGAGACTGAGTGAATCTGATCTCCATCTCCATCTGTGTGGCGGG 838
 Db 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180

```
QY 839 AACGACGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGAGAGTGCACCAAGGAG 898
DB 181 AenAspArgValGlnThrIleThrGlnLeuGluAspSerArgValThrIlysGlu 200
QY 899 AATACCCACCGTGAAGGAGGAGTGTAGTGAAGTTTGACACCTCTACGCCATCTGT 958
DB 201 AenSerHisGlnValIysGluGluSerGlnIysPheAspThrLeuTyAlaIleLeu 220
QY 959 GATGAGAAGACGAGCGAGTGTCTGACGGGATCCAGCAGGAGCAGGAGGAGTGGGC 1018
DB 221 AspGluIysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluIysLeuSer 240
QY 1019 TTCATCGAGGCTCTCATCTCCAGTACAGGAGCAGCTGGAAAGTCCACCAAGTTGTG 1078
DB 241 PheIleGluAlaLeuIleGlnIlyrGlnGluGlnLeuAspLysSerThrIysLeuVal 260
QY 1079 GAGACCGCATCCAGTCTCTGATGAGCCGAGGGGCTACCTCTCAAGTGGCCAG 1138
DB 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAAGCATTTAGAACCTCCAGGCTCCAGCTGGGAAGACAGACAA 1198
DB 281 GlnLeuIleLysSerIleValGluAlaSerIysGlyCysGlnLeuGlyIysThrGluGln 300
QY 1199 GCGTTTGAGAACATCGACTTCTTACTCTGGACTTAGAACACATAGCAGGCGCTTGAGG 1258
DB 301 GlyPheGluAenMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
QY 1259 GCCATTGACTTGGGACA 1276
DB 321 AlaIleAspPheGlyThr 326
RESULT 7
ADE61549
ID ADE61549 standard; protein; 353 AA.
AC ADE61549;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q969Q1, SEQ ID NO 7469.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO ) GEN HOSPITAL CORP.
PA (PARB ) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
```

```
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 353 AA;
```

```
Alignment Scores:
Pred. No.: 1,77e-130 Length: 353
Score: 1613.00 Matches: 305
Percent Similarity: 97.55% Conservative: 13
Best Local Similarity: 93.56% Mismatches: 8
Query Match: 56.64% Indels: 0
DB: 7 Gaps: 0
```

US-10-775-649-5 (1-1597) x ADE61549 (1-353)

```
QY 299 ATGGATTATAAATCTAGCCTGATTCCTGATGAAACGCTATGAGAACCTGGAGAAGCAG 358
DB 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCCATCTGCTGAGATGTTTACCAAGCCTGTGGTCTATCTGCTCCCTGCCNA 418
DB 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACACCTCTGCGGAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTACTGGACC 478
DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr 60
QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGAGAGTCTTTCCGTTGCCCTCGTCGCCCAT 538
DB 61 SerArgGlySerSerValSerMetSerGlyIysArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTGATCATGACCGGACGCGGTGTACCGCTTCGAGAGAACCTGCTGTGGAAAC 598
DB 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGGAGTCTCCAGTGGCCCTTCGACAAAGGAGCCACCCG 658
DB 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGluIysGlySerHisPro 120
QY 659 ATGTCAAGGAACACGAAGACGAGAAGATCAACATCTACTGTCTCAGCTGTGAGTGCCT 718
DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTTGTGCAAGGTGTTTGGGCTCACAGGCTGTGAGGTGCCCTTTCGAA 778
DB 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACAGACAGACTGAGTGAAGTAACTGCATCTCCATGCTGTGTGGCGG 838
DB 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
```

```
QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGCGAGAGTGACCAAGGAG 898
DB 181 ASnAspArgValGlnThrIleThrGlnLeuGluAspSerArgValThrLysGlu 200
QY 899 AATAGCCACGAGTGAAGGAGGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCCTG 958
DB 201 ASnSerHisGlnValLysGluGluLeuSerGlnLysPheAspThrLeuTyAlaIleLeu 220
QY 959 GATGAGAAGAGGAGGAGCTGCTGCAGCGGATCACGACGAGGAGGAGGAGCTGGGC 1018
DB 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnLysLysLeuSer 240
QY 1019 TTCTATCGAGGCTCGATCTCTCCAGTACAGGAGCAGCTGAAAAGTCCACCAAGCTTG 1078
DB 241 PheIleGluAlaLeuLeuGlnGlnTyGlnGluGlnLeuAspLysSerThrLysLeuVal 260
QY 1079 GAGACCGCCATCCAGTCCCTCGATAGCCGCGAGGGGCTACCTCTCTCAAGTGCACAG 1138
DB 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAGAGCATTTGAGAGCTCCAGAGGCTGCCAGGCTGCCAGTGGGGAAGACAGCAA 1198
DB 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GGCTTTGAGAACATGGACTACTTTACTCTGGACTTAGAACACATAGCAGAGGCTTGAGG 1258
DB 301 GlyPheGluAsnMetAspPhePheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
DB 321 AlaIleAspPheGlyThr 326
RESULT 8
ADE61546
ID ADE61546 standard; protein; 353 AA.
XX
AC ADE61546;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q969Q1, SEQ ID NO 7466.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
PA
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX
DR New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
```

```
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 353 AA;
```

Alignment Scores:

```
Pred. No.: 1.77e-130 Length: 353
Score: 1613.00 Matches: 305
Percent Similarity: 97.55% Conservative: 13
Best Local Similarity: 93.56% Mismatches: 8
Query Match: 56.64% Indels: 0
DB: 7 Gaps: 0
```

US-10-775-649-5 (1-1597) x ADE61546 (1-353)

```
QY 299 ATGGATTATAATCTAGCCTGATCTCTGATGAAGACGCTATCGAGAACCTGGAGAGCAG 358
DB 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCTCATCTCGCTCCCAA 418
DB 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACCTCTCGCGAAGTGTCCCAACGACATCTTCAGGCTGCGAATCCCTACTCGACC 478
DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGCGTGGCTCAGTGTCCATGTCGAGGTGCTTTCGTTGCCCTCGTCGCGCCAT 538
DB 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTGATCATGGACCGGCACCGGGTGTA CGGCCTGCAGAGGAACCTGCTGTGGAAAC 598
DB 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsn 100
QY 599 ATCATTGACATCTACAGCAGGAGTGCTCCAGTCGGCCCTCGAGAAAGCGACGCCG 658
DB 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGAACAGACGAGAGATCAACATCTACTGTCTACGCTGAGGGTGCCT 718
DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTTGCAAGGTGTTTGGGGCTCACCGCCTGTGAGGTCCCTTTGCCAA 778
DB 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACAGAGACTGAGTGAGTAAGTATCTCCATGCTGTGTGGCGGG 838
DB 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
```

Qy	839	AACGACCGAGTGCAGAGCATCTCTCAGCTGGAGGACTCGTGACAGAGTGACCAAGGAG	898	07-JUL-2000; 2000US-02115880P
Db	181	AsnAspArgValGlnThrIleThrGlnLeuGluAspSerArgArgValThrLysGlu	200	11-JUL-2000; 2000US-02117487P
Qy	899	AATAGCCACCAAGTGCAGGAGGAGCTGAGTCAGAGAGTTTCACACCCCTCTACGCCATCCCTG	958	11-JUL-2000; 2000US-02117496P
Db	201	AsnSerHisGlnValLysGluGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220	14-JUL-2000; 2000US-02182909P
Qy	959	GATCAGAAAGACGACGAGCTGCTCCAGCGGATCACGACGAGGAGGAGAGAGCTGGGC	1018	14-JUL-2000; 2000US-0220963P
Db	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGluLysLysLeuSer	240	26-JUL-2000; 2000US-0220964P
Qy	1019	TTTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGCTG	1078	14-AUG-2000; 2000US-0224518P
Db	241	PheIleGluAlaLeuIleGlnGlnTyrGlnGlnLysSerThrLysLeuVal	260	14-AUG-2000; 2000US-0224519P
Qy	1079	GAGACCGCCATCCAGTCCCTGGATGAGCCGCGGAGGGCTACCTCTCTCAAGTCCGAC	1138	14-AUG-2000; 2000US-0225213P
Db	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuThrAlaLys	280	14-AUG-2000; 2000US-0225214P
Qy	1139	CAGCTCATCAAGACATGTAGAACCTCCAAAGGGCTCCAGGGCTGCGGGAAGACAGAGCAA	1198	14-AUG-2000; 2000US-0225256P
Db	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300	14-AUG-2000; 2000US-0225257P
Qy	1199	GGCTTTGAGAACATGAGTACTTCTTCTGACTTAGAACACATAGCAGAGCGCTTGAGG	1258	14-AUG-2000; 2000US-0225258P
Db	301	GlyPheGluAsnMetAspPhePheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg	320	18-AUG-2000; 2000US-0226279P
Qy	1259	GCCATTGACTTTGGGACA	1276	22-AUG-2000; 2000US-0226281P
Db	321	AlaIleAspPheGlyThr	326	22-AUG-2000; 2000US-0226868P
RESULT 9				
ID	AAU15855	standard; protein; 366 AA.		
XX	AC	AAU15855;		
XX	AC	AAU15855;		
DT	07-NOV-2001	(first entry)		
XX	DE	Human novel secreted protein, Seq ID 808.		
XX	KW	Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;		
KW	KW	cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;		
KW	KW	antibacterial; virucide; fungicide; ophthalmologic; vulnerary;		
KW	KW	secreted protein; rheumatoid arthritis; hyperproliferative disorder;		
KW	KW	cardiovascular disorder; cardiac arrest; cerebrovascular disorder;		
KW	KW	cerebral ischaemia; angiogenesis; nervous system disorder;		
KW	KW	Alzheimer's disease; infection; ocular disorder; corneal infection;		
KW	KW	wound healing; epithelial cell proliferation; skin ageing; food additive;		
XX	XX	preservative; antiproliferative.		
OS		Homo sapiens.		
XX	XX	WO200155322-A2.		
XX	XX	02-AUG-2001.		
XX	XX	17-JAN-2001; 2001WO-US001341.		
XX	XX	31-JAN-2000; 2000US-0179065P.		
PR	PR	04-FEB-2000; 2000US-0180628P.		
PR	PR	24-FEB-2000; 2000US-0184664P.		
PR	PR	02-MAR-2000; 2000US-0186350P.		
PR	PR	16-MAR-2000; 2000US-0189874P.		
PR	PR	17-MAR-2000; 2000US-0190076P.		
PR	PR	18-APR-2000; 2000US-0198123P.		
PR	PR	19-MAY-2000; 2000US-0205515P.		
PR	PR	07-JUN-2000; 2000US-0209467P.		
PR	PR	28-JUN-2000; 2000US-0214886P.		
PR	PR	30-JUN-2000; 2000US-0215135P.		
PR	PR	07-JUL-2000; 2000US-0216647P.		
PR	PR	20-OCT-2000; 2000US-0241785P.		
PR	PR	20-OCT-2000; 2000US-0241786P.		
PR	PR	20-OCT-2000; 2000US-0241787P.		
PR	PR	20-OCT-2000; 2000US-0241808P.		
PR	PR	20-OCT-2000; 2000US-0241809P.		
PR	PR	20-OCT-2000; 2000US-0241810P.		
PR	PR	20-OCT-2000; 2000US-0241811P.		
PR	PR	20-OCT-2000; 2000US-0241812P.		
PR	PR	20-OCT-2000; 2000US-0241813P.		
PR	PR	20-OCT-2000; 2000US-0241814P.		
PR	PR	20-OCT-2000; 2000US-0241815P.		
PR	PR	20-OCT-2000; 2000US-0241816P.		
PR	PR	20-OCT-2000; 2000US-0241817P.		
PR	PR	20-OCT-2000; 2000US-0241818P.		
PR	PR	20-OCT-2000; 2000US-0241819P.		
PR	PR	20-OCT-2000; 2000US-0241820P.		
PR	PR	20-OCT-2000; 2000US-0241821P.		
PR	PR	20-OCT-2000; 2000US-0241822P.		
PR	PR	20-OCT-2000; 2000US-0241823P.		
PR	PR	20-OCT-2000; 2000US-0241824P.		
PR	PR	20-OCT-2000; 2000US-0241825P.		
PR	PR	20-OCT-2000; 2000US-0241826P.		
PR	PR	20-OCT-2000; 2000US-0241827P.		
PR	PR	20-OCT-2000; 2000US-0241828P.		
PR	PR	20-OCT-2000; 2000US-0241829P.		
PR	PR	20-OCT-2000; 2000US-0241830P.		
PR	PR	20-OCT-2000; 2000US-0241831P.		
PR	PR	20-OCT-2000; 2000US-0241832P.		
PR	PR	20-OCT-2000; 2000US-0241833P.		
PR	PR	20-OCT-2000; 2000US-0241834P.		
PR	PR	20-OCT-2000; 2000US-0241835P.		
PR	PR	20-OCT-2000; 2000US-0241836P.		
PR	PR	20-OCT-2000; 2000US-0241837P.		
PR	PR	20-OCT-2000; 2000US-0241838P.		
PR	PR	20-OCT-2000; 2000US-0241839P.		
PR	PR	20-OCT-2000; 2000US-0241840P.		
PR	PR	20-OCT-2000; 2000US-0241841P.		
PR	PR	20-OCT-2000; 2000US-0241842P.		
PR	PR	20-OCT-2000; 2000US-0241843P.		
PR	PR	20-OCT-2000; 2000US-0241844P.		
PR	PR	20-OCT-2000; 2000US-0241845P.		
PR	PR	20-OCT-2000; 2000US-0241846P.		
PR	PR	20-OCT-2000; 2000US-0241847P.		
PR	PR	20-OCT-2000; 2000US-0241848P.		
PR	PR	20-OCT-2000; 2000US-0241849P.		
PR	PR	20-OCT-2000; 2000US-0241850P.		
PR	PR	20-OCT-2000; 2000US-0241851P.		
PR	PR	20-OCT-2000; 2000US-0241852P.		
PR	PR	20-OCT-2000; 2000US-0241853P.		
PR	PR	20-OCT-2000; 2000US-0241854P.		
PR	PR	20-OCT-2000; 2000US-0241855P.		
PR	PR	20-OCT-2000; 2000US-0241856P.		
PR	PR	20-OCT-2000; 2000US-0241857P.		
PR	PR	20-OCT-2000; 2000US-0241858P.		
PR	PR	20-OCT-2000; 2000US-0241859P.		
PR	PR	20-OCT-2000; 2000US-0241860P.		
PR	PR	20-OCT-2000; 2000US-0241861P.		
PR	PR	20-OCT-2000; 2000US-0241862P.		
PR	PR	20-OCT-2000; 2000US-0241863P.		
PR	PR	20-OCT-2000; 2000US-0241864P.		
PR	PR	20-OCT-2000; 2000US-0241865P.		
PR	PR	20-OCT-2000; 2000US-0241866P.		
PR	PR	20-OCT-2000; 2000US-0241867P.		
PR	PR	20-OCT-2000; 2000US-0241868P.		
PR	PR	20-OCT-2000; 2000US-0241869P.		
PR	PR	20-OCT-2000; 2000US-0241870P.		
PR	PR	20-OCT-2000; 2000US-0241871P.		
PR	PR	20-OCT-2000; 2000US-0241872P.		
PR	PR	20-OCT-2000; 2000US-0241873P.		
PR	PR	20-OCT-2000; 2000US-0241874P.		
PR	PR	20-OCT-2000; 2000US-0241875P.		
PR	PR	20-OCT-2000; 2000US-0241876P.		
PR	PR	20-OCT-2000; 2000US-0241877P.		
PR	PR	20-OCT-2000; 2000US-0241878P.		
PR	PR	20-OCT-2000; 2000US-0241879P.		
PR	PR	20-OCT-2000; 2000US-0241880P.		
PR	PR	20-OCT-2000; 2000US-0241881P.		
PR	PR	20-OCT-2000; 2000US-0241882P.		
PR	PR	20-OCT-2000; 2000US-0241883P.		
PR	PR	20-OCT-2000; 2000US-0241884P.		
PR	PR	20-OCT-2000; 2000US-0241885P.		
PR	PR	20-OCT-2000; 2000US-0241886P.		
PR	PR	20-OCT-2000; 2000US-0241887P.		
PR	PR	20-OCT-2000; 2000US-0241888P.		
PR	PR	20-OCT-2000; 2000US-0241889P.		
PR	PR	20-OCT-2000; 2000US-0241890P.		
PR	PR	20-OCT-2000; 2000US-0241891P.		
PR	PR	20-OCT-2000; 2000US-0241892P.		
PR	PR	20-OCT-2000; 2000US-0241893P.		
PR	PR	20-OCT-2000; 2000US-0241894P.		
PR	PR	20-OCT-2000; 2000US-0241895P.		
PR	PR	20-OCT-2000; 2000US-0241896P.		
PR	PR	20-OCT-2000; 2000US-0241897P.		
PR	PR	20-OCT-2000; 2000US-0241898P.		
PR	PR	20-OCT-2000; 2000US-0241899P.		
PR	PR	20-OCT-2000; 2000US-0241900P.		
PR	PR	20-OCT-2000; 2000US-0241901P.		
PR	PR	20-OCT-2000; 2000US-0241902P.		
PR	PR	20-OCT-2000; 2000US-0241903P.		
PR	PR	20-OCT-2000; 2000US-0241904P.		
PR	PR	20-OCT-2000; 2000US-0241905P.		
PR	PR	20-OCT-2000; 2000US-0241906P.		
PR	PR	20-OCT-2000; 2000US-0241907P.		
PR	PR	20-OCT-2000; 2000US-0241908P.		
PR	PR	20-OCT-2000; 2000US-0241909P.		
PR	PR	20-OCT-2000; 2000US-0241910P.		
PR	PR	20-OCT-2000; 2000US-0241911P.		
PR	PR	20-OCT-2000; 2000US-0241912P.		
PR	PR	20-OCT-2000; 2000US-0241913P.		
PR	PR	20-OCT-2000; 2000US-0241914P.		
PR	PR	20-OCT-2000; 2000US-0241915P.		
PR	PR	20-OCT-2000; 2000US-0241916P.		
PR	PR	20-OCT-2000; 2000US-0241917P.		
PR	PR	20-OCT-2000; 2000US-0241918P.		
PR	PR	20-OCT-2000; 2000US-0241919P.		
PR	PR	20-OCT-2000; 2000US-0241920P.		
PR	PR	20-OCT-2000; 2000US-0241921P.		
PR	PR	20-OCT-2000; 2000US-0241922P.		
PR	PR	20-OCT-2000; 2000US-0241923P.		
PR	PR	20-OCT-2000; 2000US-0241924P.		
PR	PR	20-OCT-2000; 2000US-0241925P.		
PR	PR	20-OCT-2000; 2000US-0241926P.		
PR	PR	20-OCT-2000; 2000US-0241927P.		
PR	PR	20-OCT-2000; 2000US-0241928P.		
PR	PR	20-OCT-2000; 2000US-0241929P.		
PR	PR	20-OCT-2000; 2000US-0241930P.		
PR	PR	20-OCT-2000; 2000US-0241931P.		
PR	PR	20-OCT-2000; 2000US-0241932P.		
PR	PR	20-OCT-2000; 2000US-0241933P.		
PR	PR	20-OCT-2000; 2000US-0241934P.		
PR	PR	20-OCT-2000; 2000US-0241935P.		
PR	PR	20-OCT-2000; 2000US-0241936P.		
PR	PR	20-OCT-2000; 2000US-0241937P.		
PR	PR	20-OCT-2000; 2000US-0241938P.		
PR	PR	20-OCT-2000; 2000US-0241939P.		
PR	PR	20-OCT-2000; 2000US-0241940P.		
PR	PR	20-OCT-2000; 2000US-0241941P.		
PR	PR	20-OCT-2000; 2000US-0241942P.		
PR	PR	20-OCT-2000; 2000US-0241943P.		
PR	PR	20-OCT-2000; 2000US-0241944P.		
PR	PR	20-OCT-2000; 2000US-0241945P.		
PR	PR	20-OCT-2000; 2000US-0241946P.		
PR	PR	20-OCT-2000; 2000US-0241947P.		
PR	PR	20-OCT-2000; 2000US-0241948P.		
PR	PR	20-OCT-2000; 2000US-0241949P.		
PR	PR	20-OCT-2000; 2000US-0241950P.		
PR	PR	20-OCT-2000; 2000US-0241951P.		
PR	PR	20-OCT-2000; 2000US-0241952P.		
PR	PR	20-OCT-2000; 2000US-0241953P.		
PR	PR	20-OCT-2000; 2000US-0241954P.		
PR	PR	20-OCT-2000; 2000US-0241955P.		
PR	PR	20-OCT-2000; 2000US-0241956P.		
PR	PR	20-OCT-2000; 2000US-0241957P.		
PR	PR	20-OCT-2000; 2000US-0241958P.		
PR	PR	20-OCT-2000; 2000US-0241959P.		
PR	PR	20-OCT-2000; 2000US-0241960P.		
PR	PR	20-OCT-2000; 2000US-0241961P.		
PR	PR	20-OCT-2000; 2000US-0241962P.		
PR	PR	20-OCT-2000; 2000US-0241963P.		
PR	PR	20-OCT-2000; 2000US-0241964P.		
PR	PR	20-OCT-2000; 2000US-0241965P.		
PR	PR	20-OCT-2000; 2000US-0241966P.		
PR	PR	20-OCT-2000; 2000US-0241967P.		
PR	PR	20-OCT-2000; 2000US-0241968P.		
PR	PR	20-OCT-2000; 2000US-0241969P.		
PR	PR	20-OCT-2000; 2000US-0241970P.		
PR	PR	20-OCT-2000; 2000US-0241971P.		
PR	PR	20-OCT-2000; 2000US-0241972P.		
PR	PR	20-OCT-2000; 2000US-0241973P.		
PR	PR	20-OCT-2000; 2000US-0241974P.		
PR	PR	20-OCT-2000; 2000US-0241975P.		
PR	PR	20-OCT-2000; 2000US-0241976P.		
PR	PR	20-OCT-2000; 2000US-0241977P.		
PR	PR	20-OCT-2000; 2000US-0241978P.		
PR	PR	20-OCT-2000; 2000US-0241979P.		
PR	PR	20-OCT-2000; 2000US-0241980P.		

PR	01-SEP-2000;	2000US-0229343P.			
PR	01-SEP-2000;	2000US-0229344P.			
PR	01-SEP-2000;	2000US-0229345P.			
PR	05-SEP-2000;	2000US-0229509P.			
PR	05-SEP-2000;	2000US-0229513P.			
PR	08-SEP-2000;	2000US-0231413P.			
PR	21-SEP-2000;	2000US-0234223P.			
PR	21-SEP-2000;	2000US-0234274P.			
PR	25-SEP-2000;	2000US-0234977P.			
PR	27-SEP-2000;	2000US-0235834P.			
PR	29-SEP-2000;	2000US-0236327P.			
PR	29-SEP-2000;	2000US-0236367P.			
PR	29-SEP-2000;	2000US-0236368P.			
PR	29-SEP-2000;	2000US-0236369P.			
PR	29-SEP-2000;	2000US-0236370P.			
PR	02-OCT-2000;	2000US-0236802P.			
PR	02-OCT-2000;	2000US-0237037P.			
PR	02-OCT-2000;	2000US-0237038P.			
PR	02-OCT-2000;	2000US-0237039P.			
PR	02-OCT-2000;	2000US-0237040P.			
PR	13-OCT-2000;	2000US-0239935P.			
PR	20-OCT-2000;	2000US-0240960P.			
PR	20-OCT-2000;	2000US-0241785P.			
PR	20-OCT-2000;	2000US-0241809P.			
PR	01-NOV-2000;	2000US-0244617P.			
PR	17-NOV-2000;	2000US-0249299P.			
PR	08-DEC-2000;	2000US-0251856P.			
PR	08-DEC-2000;	2000US-0251868P.			
PR	08-DEC-2000;	2000US-0251869P.			
XX					
PA	(ROSE/) ROSEN C A.				
PA	(RUBE/) RUBEN S M.				
PA	(BARA/) BARASH S C.				
XX					
PI	Rosen CA, Ruben SM, Barash SC;				
XX					
DR	WPI; 2003-147444/14.				
DR	N-PSDE; ABX73183.				
XX					
PT	New polypeptides and nucleic acids, useful in gene therapy for treating,				
PT	inhibiting or preventing e.g. neural, immune system, muscular, or				
PT	respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or				
PT	renal disorders.				
XX					
PS	Claim 11; SEQ ID NO 808; 402pp; English.				
XX					
CC	The invention relates to human novel polypeptides and their associated				
CC	polynucleotides. The polypeptides and polynucleotides are useful in gene				
CC	therapy for treating, inhibiting or preventing neural disorders, immune				
CC	system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis				
CC	and multiple sclerosis), muscular disorders, respiratory diseases (e.g.				
CC	nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,				
CC	gastrointestinal disorders, pulmonary disorders, cardiovascular disorders				
CC	(e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left				
CC	heart syndrome), renal disorders (e.g. acute kidney failure and end-stage				
CC	renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and				
CC	leukaemia), inflammatory diseases (e.g. septic shock, bursitis and				
CC	appendicitis), allergic reactions and conditions (e.g. asthma), blood				
CC	related disorders (e.g. thrombosis, atherosclerosis and myocardial				
CC	infarction) and cancerous diseases. Sequences ABU54914-ABU55699 and				
CC	ABU55748 represent human novel polypeptides of the invention				
XX					
SQ	Sequence 366 AA;				
	Alignment Scores:				
	Pred. No.:	1.99e-130	Length:		366
	Score:	1612.50	Matches:		308
	Percent Similarity:	94.19%	Conservative:		16
	Best Local Similarity:	89.53%	Mismatches:		15
	Query Match:	56.82%	Indels:		5
	DB:	6	Gaps:		1
	US-10-775-649-5 (1-1597) x ABU54924 (1-366)				

DB:	4	Gaps:	1
US-10-775-649-5 (1-1597) x AAU25438 (1-366)			
QY	245	AGACAAAGACTTGTGTGACGACGAGTGGCGCAAGACAGTCGCATTTCAAAGCAATATGATG	304
Db	1	ArgargGlnLeuGlyValAlaLeuLeuPro-----SerHisArgMetAsp	15
QY	305	TATAAATCTAGCCTGATTCTCTGATGGAAACGCTATGGAGAACCTCGGAGAGCAGCTGATC	364
Db	16	TyrLysSerSerLeuIleGlnAspGlyAAsnProMetGluAAsnLeuGluValGlnLeuIle	35
QY	365	TGCCCCATCGCTGGAGAGATGTTTACCAAGCCTGTGTCTATCCTCGCTGCTGCAACACAAC	424
Db	36	CysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGlnHisAsn	55
QY	425	CTCTCGCGGAAGTGTGCAACGACATCTCCAGAGCTCGAATCCTACTGGACCAACCGC	484
Db	56	LeuCysargLysCysAlaAsnAspIlePheGlnAlaSerAAsnProTyrLeuProThrArg	75
QY	485	GGTGGCTCAGTGTCCATGTCGTGGAGGTGCTTTCCGTTGCGCCCTCGTCGCCCATGAAGTG	544
Db	76	GlyGlyThrThrMetAlaSerGlyLysArgPheArgCysProSerCysArgHisGluVal	95
QY	545	ATCATGACCGGACCGGGGTGTACGGCTGCAGAGGAACCTGCTGGTGGGAAAAATCATCT	604
Db	96	ValLeuAspArgHisGlyValTyrGlyLeuGlnArgAAsnLeuValGluAAsnIleIle	115
QY	605	GACATCTACAGCAGGAGTGTCTCAGTCGGCCCTGCAGAAAGCGACCCACCGATGTC	664
Db	116	AspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisProMetCys	135
QY	665	AAGGAAACAAAGACGAGAAAGATCAAATCTACTGTCTCAGTGTGAGGTGCTACTTTCG	724
Db	136	LysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValProThrCys	155
QY	725	TCCTTTGTCAAAGTGTGTTGGGGCTCACACAGCCCTGTGAGGTGGCCCTTTGCAAAAGCATC	784
Db	156	SerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGlnSerVal	175
QY	785	TTTCAAGGACAGAGACTGAGCTCAGTAACATCTCCATCTGCTGGTGGGGGGAACGAC	844
Db	176	PheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGlyAsnAsp	195
QY	845	CGAGTGCAGACCATCATCTCTCAGCTGGAGACTCTGTCAGAGTGCACCAAGGAGAATAGC	904
Db	196	ArgValGlnThrIleIleThrGlnLeuGluAspSerArgValThrLysGluAsnSer	215
QY	905	CACAGGTGAAGGAGGAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCCTGGATGAG	964
Db	216	HisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeuAspGlu	235
QY	965	AAGAAGCAGGCTGCTGCAGCGGATCAGCAGGACGAGGAGGAGAGCTGGGCTTCATC	1024
Db	236	LysLysSerGluLeuLeuGlnArgIleThrGlnGlnGluLysLysLeuSerPheIle	255
QY	1025	GAGGCTGTATCTCCAGTACAGGAGCAGCTGCGAAAAGTCCACCAAGCTGTGTGGAGACC	1084
Db	256	GluAlaLeuIleGlnGlnTyrGlnGlnLeuAspLysSerThrLysLeuValGluThr	275
QY	1085	GCCATCCAGTCCCTGGATGAGCCCGGAGGGCTACCTTCCTCTCAAGTGCCACAGAGCTC	1144
Db	276	AlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLysGlnLeu	295
QY	1145	ATCAAGACCATGTAGAACCTCCAGGGCTGCCAGCTGGGGGAGACAGACAGGCTTT	1204
Db	296	IleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGlnGlyPhe	315
QY	1205	GAGAAATGTGGACTACTTTACTCTGAGACTTAGAAACATAGCAGAGCCCTTGAGGGCCATT	1264
Db	316	GluAAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArgAlaIle	335
QY	1265	GACTTTTGGGACA	1276

Db		336 AspPheGlyThr 339
RESULT 12		
ABB81135		
ID	ABB81135	standard; protein; 340 AA.
XX	ABB81135;	
XX	05-NOV-2002	(first entry)
XX	Human MURF1	protein.
XX	Muscle atrophy protein; MURF1; MURF3; MAFBX;	atrophy; neuroprotective;
KW	gene therapy; transgenic; human.	
XX	Homo sapiens.	
XX	WO200261046-A2.	
XX	08-AUG-2002.	
XX	30-JAN-2002;	2002WO-US002811.
XX	30-JAN-2001;	2001US-0264926P.
PR	10-AUG-2001;	2001US-0311637P.
PR	22-OCT-2001;	2001US-0338742P.
XX	(REGE-)	REGENERON PHARM INC.
XX	Glass DJ,	Bodine SC;
XX	WPI;	2002-608513/65.
DR	N-PSDB;	ABQ79507.
XX	Isolated nucleic acid molecules encoding muscle atrophy proteins, e.g.	
PT	MURF1, MURF3 or MAFBX, useful for treating muscle atrophy and other	
PT	related disorders, e.g. Guillian-Barre syndrome, peripheral neuropathy,	
PT	and nerve damage.	
XX	Claim 1;	Fig 9; 104pp; English.
PS	The invention relates to isolated nucleic acid molecules encoding muscle	
XX	atrophy proteins MURF1, MURF3, or MAFBX. The proteins can be expressed by	
CC	standard recombinant methodology. The nucleic acid molecules and	
CC	polypeptides are useful for treating muscle atrophy or detecting atrophy,	
CC	and for treating related diseases/disorders, e.g. Guillian-Barre	
CC	syndrome, peripheral neuropathy, or nerve damage caused by environmental	
CC	toxins or drugs. The MURF1, MURF3 and MAFBX antagonists, and the	
CC	antagonists of their pathways are useful for inhibiting atrophy, inducing	
CC	hyperatrophy, decreasing ubiquitination, interfering with the ubiquitin	
CC	pathway, or modulating MURF1, MURF3 or MAFBX expression or activity. The	
CC	nucleotide sequences are useful for diagnostic and genetic testing. The	
CC	present sequence represents a human MURF1 protein	
XX	Sequence 340 AA;	
SQ		
Alignment Scores:		
Pred. No.:	4,56e-126	Length: 340
Score:	1562.00	Matches: 295
Percent Similarity:	98.08%	Conservative: 12
Best Local Similarity:	94.25%	Mismatches: 6
Query Match:	54.85%	Indels: 0
DB:	5	Gaps: 0
US-10-775-649-5 (1-1597) x ABB81135 (1-340)		
Qy	338	ATGGAGAACCTGGAGAGACAGCTGATCTGCCCCATCTGCGAGATGTTTACCAAGCCT 397
Db	1	MetGluasnLeuGluLysGlnLeuIleCysProIleCysLeuGluMetPheThrLysPro 20
Qy	398	GTGTGTCATCTGCGCTTGCCTGCAACACAACTCTGCGCGAGAGTGTCGAACGACATCTCCAG 457

Db 111 Glu---SerThrArgProGluLysSerAspGlnProMetCysGluGluHisGluGlu 129
QY 680 GAGAGATCAACTACTCTCTCACCGTGTGAGGTGCTACTCTGCTCCCTGTCAGAGTG 739
Db 130 GluArgGlnAsnIleTyrCysLeuAsnCysGluValProThrCysSerLeuCysLysVal 149
QY 740 TTTGGGGCTCACGAGCGCTGTGAGGTGGCCCTTTGCCAAAGCATCTTCCAAGGACAGAAG 799
Db 150 PheGlyAlaHisLysAspCysGlnValAlaProLeuThrHisValPheGlnArgGlnLys 169
QY 800 ACTGAGCTAGTAACCTGATCTCCATGCTGTGGCGGGGACACGAGTGCAGAGCATC 859
Db 170 SerGluLeuSerAspGlyIleAlaIleLeuValGlySerAsnAspArgValGlnGlyVal 189
QY 860 ATCTCTCAGCTGAGGAGCTGTGCAGAGTGACCAAGAGGAATAGCACAGGTGAAGGAG 919
Db 190 IleSerGlnLeuGluAspThrCysLysThrIleGluGluCysCysArgLysGlnLysGln 209
QY 920 GAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCTGTGATGAGAAGAGCGAGCTG 979
Db 210 GluLeuCysGlnLysPheAspTyrLeuTyrGlyIleLeuGluGluArgLysAsnGluMet 229
QY 980 CTCACGGGATCAGCAGGAGGAGGAGAGCTGGCTTCATCAGAGCTCTGATCCTC 1039
Db 230 ThrGlnValIleThrArgThrGlnGluGluLysLeuGluHisValArgAlaLeuLys 249
QY 1040 CAGTACAGGAGCAGCTGGAAAGTCCACCAAGCTGTGTGAGACCGCCATCCAGTCCCTG 1099
Db 250 LysTyrSerAspHisLeuGluAsnValSerLysLeuValGluSerGlyIleGlnPheMet 269
QY 1100 GATGAGCCCGAGGGGCTACTCTTCTCTCAAGTSCCAAGCAGCTCATCAAGAGCATGTGA 1159
Db 270 AspGluProGluMetAlaValPheLeuGlnAsnAlaLysThrLeuLysLysIleSer 289
QY 1160 GAAGCTTCCAGGCTGCCAGCTGGGAGAGACAGCAAGCGCTTTCAGAACATGAGCTAC 1219
Db 290 GluAlaSerLysAlaPheGlnMetGluLysIleGluHisGlyTyrGluAsnMetAsnHis 309
QY 1220 TTTACTCTGACTTAGAACATAGCAGAGGCGCTTCGAGGCGCCATTCACCTT 1270
Db 310 PheThrValAsnLeuAsnArgGluGluLysIleIleArgGluIleAspPhe 326
RESULT 15
ADB64249
ID ADB64249 standard; protein; 452 AA.
XX
AC ADB64249;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human protein encoded by clone DFNS20073320.
XX
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX
XX Homo sapiens.
XX
XX EP1308459-A2.
XX
XX 07-MAY-2003.
XX
XX 28-MAR-2002; 2002EP-00007401.
XX
XX 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI: 2003-450961/43.
DR N-PSDB; ADB62279.
XX
PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
SQ Sequence 452 AA;

Alignment Scores:
Pred. No.: 2,79e-88 Length: 452
Score: 1126.50 Matches: 221
Percent Similarity: 67.00% Conservative: 45
Best Local Similarity: 55.67% Mismatches: 60
Query Match: 39.55% Indels: 71
DB: 7 Gaps: 2

US-10-775-649-5 (1-1597) x ADB64249 (1-452)

QY 80 ATGAGCATTCTCTGAATTACAAGTCTTTCTCCAAGAGCAGCAGCATGGATACTTG 139
Db 1 MetSerAlaSerLeuAsnTyrLysSerPheSerLysGluGlnThrMetAsp----- 18

QY 140 GAAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCCAGAGCCTGTGGTCATCTC 199
Db 18 ----- 18

QY 200 CCTTGCACGACACACCTGTGTGAGGAAATGTGCGGGGCCCCCTTGGAGACAAAGACTTGT 259
Db 18 ----- 18

QY 260 GTGACGCGAGGTGGGCAAGACAGTCGCATTTCAAAGCAATATGGAATTATAATCTAGCCTG 319
Db 18 ----- 18

QY 320 ATTCTGATGGAACGCTATGGAGAACCTGGAGAGACAGCTGATCTGCCCATCTGCTGCTG 379
Db 19 -----AsnLeuGluLysGlnLeuLeuCysProIleCysLeu 30

QY 380 GAGATGTTTACCAAGCCTGTGGTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 439
Db 31 GluMetPheThrLysProValValIleLeuProCysGlnHisAsnLeuLysArgLysCys 50

QY 440 GCCAAGACATCTTCCAGGCTCGGAATCCCTACTGTGACCAACCGCGGTGGCTCAGTGTC 499

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	432.5	15.2	667	2	T09482	ring finger protein
2	426.5	15.0	667	2	T09013	RING finger protein
3	281.5	9.9	609	2	A43906	nuclear phosphopro
4	255.5	9.0	551	2	JC7562	glioblastoma RING
5	255.5	9.0	792	2	T00082	hypothetical prote
6	243	8.5	624	2	S28418	probable zinc-bind
7	235	8.3	518	2	JC7387	testis-abundant fi
8	234.5	8.2	365	2	A30891	regulatory protein
9	232.5	8.2	513	1	TVHURE	ret finger protein
10	232.5	8.2	801	4	TVHURE	transforming prote
11	229.5	8.1	506	2	S37583	RING finger protein
12	225.5	7.9	477	2	JE0343	tef protein - rat
13	208	7.3	442	2	A57041	transcription regu
14	193.5	6.8	375	2	F88947	protein C39P7.2 [i

Qy	458	GCTCGGAATCCCTACTGGAACCAACGGCGGTGGCTCAGTGTCCATGTCTGGAGGTGCTTTC	517
Db	39	---ValSerHisCysAlaThrAsnGlu-----SerValGlu---SerIleThrAlaPhe	54
Qy	518	CGTTGCGCCCTCGTCGGCCATGAAGTGATCATGACCGGCACGGGTGTACGGCTCGAC	577
Db	55	GlnCysProThrCysArgHisValIleThrLysSerGlnArgGlyLeuAspGlyLeuLys	74
Qy	578	AGGAACCTGCTGGTGGAAAAATCATTTACACATCTACAAAG-----	616
Db	75	ArgAsnValThrLeuGlnAsnIleIleAspArgPheGlnLysAlaSerValSerGlyPro	94
Qy	616	-----	616
Db	95	AsnSerProSerGluThrArgArgGluArgAlaPheAspAlaAsnThrMetThrSerAla	114
Qy	617	-----CAGGAGTGTCCAGTCGGCCCTCGAC-----	643
Db	115	GluLysValLeuCysGlnPheCysAspGlnAspProAlaGlnAspAlaValLysThrCys	134
Qy	644	-----AAAGCAGCCACCCG-----	658
Db	135	ValThrCysGluValSerTyrCysAspGluCysLeuLysAlaThrHisProAsnLysLys	154
Qy	659	-----ATG	661
Db	155	ProPheThrGlyHisArgLeuIleGluProfileProAspSerHisIleArgGlyLeuMet	174
Qy	662	TGCAAGGAACACGAAGACGAGAAGATCAACATCTACTGTCTCAGCTGTGAGGTCCCTACT	721
Db	175	CysLeuGluHisGluAspGluLysValAsnMetTyrCysValThrAspAspGluLeuIle	194
Qy	722	TGCTCCTTGTGCAAGGTGTTTGGGGCTCACACAGCCCTGTGAGGTGGCCCTTTCCAAAGC	781
Db	195	CysAlaLeuCysLysLeuValGlyArgHisArgAspHisGlnValAlaAlaLeuSerGlu	214
Qy	782	ATCTTCCAGGACAGAAGACTGACTGAGTAACTGCATCTCCATCTGTGTGGCGGGGAAC	841
Db	215	ArgTyrAspLysLeuLysGlnAsnLeuGluSerAsnLeuThrAsnLeuIleLysArgAsn	234
Qy	842	GACCGAGTGACAGCATCATCTCTCAGCTGGAGGACTCGTGACAGTGCACCAAGGAGAAAT	901
Db	235	ThrGluLeuGluThrLeuLeuAlaLysLeuIleGlnThrCysGlnHisValGluValAsn	254
Qy	902	AGCCACCGAGTGAAGGAGGACTGAGTCAGAAGTTTCACACCTCTCTACGCCATCTCGAT	961
Db	255	AlaSerArgGlnGluAlaLysLeuThrGluGluCysAspLeuLeuIleGluIleIleGln	274
Qy	962	GAGAAGAAGACGAGCTGCTCCACGGCATCACGAGGACGAGGAGGAGAGTCTGGCTTC	1021
Db	275	GlnArgGlnIleIleGlyThrLysIleLysGluGlyLysValMetArgLeuArgLys	294
Qy	1022	ATCAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAAAAGTCCACCAAGCTGTGGAG	1081
Db	295	LeuAlaGlnGlnIleAlaAsnCysLysGlnCysIleGluArgSerAlaSerLeuIleSer	314
Qy	1082	ACGCCCATCAGTCCCTGGATGACGCCGGAGGGGCTACCTTCTCTCAAGTGCCCAAGCAG	1141
Db	315	GlnAlaGluHisSerLeuLysGluAsnAspHisAlaArgPheLeuGlnThrAlaLysAsn	334
Qy	1142	CTCATCAAGAGCATTTAGAACCTCCACGGCTGCCAGCTGGGGGAACAGACGACGAGGC	1201
Db	335	IleThrGluArgValSerMetAlaThrAlaSerSerGlnValLeuIleProGluIleAsn	354
Qy	1202	TTT---GAGAACATGTGACTTCTTCTCTGGACTTAGAACACATAGCAGAGCCCTCAGG	1258
Db	355	LeuAsnAspThrPheAspThrPheAlaLeuAspPheSerArgGluLysLysLeuLeuGlu	374
Qy	1259	GCCATTGACTTTGGGACA	1276
Db	375	CysLeuAspTyrLeuThr	380

```

RESULT 2
T09013
RING finger protein Fxy - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 04-Apr-2004
C:Accession: T09013
R:Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
A:Title: A gene spans the pseudautosomal boundary in mice.
A:Reference number: Z16531; MUID:98004518; PMID:9342357
A:Accession: T09013
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-567 <PAL>
A:Cross-references: EMBL:AF026565; NID:G2589222; PIDN:AAB83986.1; PID:G2589223
C:Genetics:
A:Gene: Fxy
A:Map position: X; Y
C:Superfamily: rfp transforming protein
C:Keywords: zinc finger
F:6-65/Domain: RING finger homology <RRN>

Alignment Scores:
Pred. No.: 3 73e-23
Score: 426.50
Percent Similarity: 46.11%
Best Local Similarity: 27.20%
Query Match: 14.98%
DB: 2
Gaps: 7

```

Qy 722 TGCTCCTTGTCGAAGGTGTTTGGGGCTCACACGGCCTGTGAGGTTGCCCCCTTTTGCAAAGC 781

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 15, 2005, 12:34:11 ; Search time 163 Seconds
(without alignments)
10034.239 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 2848

Sequence: 1 ctcgagattacccttacg.....gaaataaattatctctgtgcc 1597

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p,model -DEV=xlp
-Q=/cgn2.1/USPTO.spool.p/US10775649/runat.14062005.141110.20658/app_query.fasta_1.1735
-DB=UniProt_03 -QFWI=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFWT=ptp -NORM=ext -HRAPSIZB=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10775649 @CGN 1.1.159 @runat.14062005.141110.20658 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=1120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1671	58.7	351	Q91Z63	Q91Z63 rattus norv
2	1613	56.6	346	Q6NR77	Q6NR77 homo sapien
3	1613	56.6	353	1 RN28 HUMAN	Q6NR77 homo sapien
4	1188.5	41.7	356	2 Q6DE39	Q6DE39 xenopus lae
5	1126.5	39.6	540	2 Q81UD9	Q81UD9 homo sapien
6	1120.5	39.3	360	2 Q6INV6	Q6INV6 xenopus lae
7	1119.5	39.3	452	2 Q96DV3	Q96DV3 homo sapien
8	1119.5	39.3	548	2 Q96DV2	Q96DV2 homo sapien
9	1110	39.0	366	2 Q9ERP3	Q9ERP3 mus musculu
10	1093.5	38.4	436	1 RN29 HUMAN	Q9ERP3 mus musculu
11	1093.5	38.4	532	2 Q9BYV5	Q9BYV5 homo sapien
12	1092.5	38.4	342	2 Q9BYV3	Q9BYV5 homo sapien
13	1062.5	37.3	384	2 Q9BYV2	Q9BYV3 homo sapien
14	1036.5	36.4	443	2 Q6DHS0	Q9BYV2 homo sapien
15	933	32.8	345	2 Q6IQH8	Q6DHS0 brachydanio
16	914.5	32.1	348	2 Q7ZWH0	Q6IQH8 brachydanio
					Q7ZWH0 brachydanio

ALIGNMENTS

RESULT 1

ID	Q91Z63	PRELIMINARY;	PRT;	351 AA.
AC	Q91Z63;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Muscle ring finger protein 1 (Ring finger protein 28).			
GN	Name=Rnf28;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RX	MEDLINE=21578247; PubMed=11679633; DOI=10.1126/science.1065874;			
RA	Bodine S.C., Latres E., Baumhueter S., Lai V.K.-M., Nunez L.,			
RA	Clarke B.A., Poueymirou W.T., Panaro F.J., Na B., Dharmarajan K.,			
RA	Pan Z.-Q., Valenzuela D.M., DeChiara T.M., Stitt T.N.,			
RA	Yancopoulos G.D., Glass D.J.;			
RT	"Identification of ubiquitin ligases required for skeletal muscle atrophy."			
RL	Science 294:1704-1708(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			

17	862.5	30.3	225	2	Q9GMX4	Q9GMX4 macaca fasc
18	831.5	29.2	241	2	Q8IUE4	Q8IUE4 homo sapien
19	820.5	28.8	197	2	Q8C6Y1	Q8C6Y1 mus musculu
20	807	28.3	429	2	Q6DC78	Q6DC78 brachydanio
21	611.5	21.5	151	2	Q8BWC4	Q8BWC4 mus musculu
22	457.5	16.1	498	2	Q6NT41	Q6NT41 homo sapien
23	455	16.0	524	2	Q6ZRL7	Q6ZRL7 homo sapien
24	453.5	15.9	498	2	Q6NT17	Q6NT17 homo sapien
25	448.5	15.7	498	2	Q9BGS5	Q9BGS5 macaca fasc
26	447	15.7	551	2	Q9H5P2	Q9H5P2 homo sapien
27	447	15.7	759	2	Q724K8	Q724K8 homo sapien
28	442	15.5	644	2	Q95J41	Q95J41 macaca fasc
29	441	15.5	441	2	Q64LM2	Q64LM2 mus musculu
30	441	15.5	759	2	Q7TNM2	Q7TNM2 mus musculu
31	435	15.3	693	2	Q6PH04	Q6PH04 brachydanio
32	434.5	15.3	667	1	MID1 RAT	P82458 rattus norv
33	433.5	15.2	667	2	Q71R46	Q71R46 gallus gall
34	433	15.2	424	2	Q6P119	Q6P119 mus musculu
35	432.5	15.2	667	1	MID1 HUMAN	Q15344 homo sapien
36	432.5	15.2	680	1	Q90WD1	Q90WD1 gallus gall
37	432.5	15.2	680	1	MID1 MOUSE	Q70583 mus musculu
38	432	15.2	668	2	Q6DEU6	Q6DEU6 xenopus tro
39	426	15.0	729	2	Q7TNM1	Q7TNM1 mus musculu
40	425	14.9	728	2	Q9NQ86	Q9NQ86 homo sapien
41	424.5	14.9	667	1	MID1 MUSSP	P82457 mus spretus
42	418	14.7	733	2	Q6NU77	Q6NU77 xenopus lae
43	407	14.3	729	2	Q80WG7	Q80WG7 mus musculu
44	402.5	14.1	685	1	MID2 MOUSE	Q9QU86 mus musculu
45	402.5	14.1	685	2	Q6GX19	Q6GX19 aotus trivi

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AY059627; AL16405.1; -.
DR EMBL; BC061824; AAH61824.1; -.
DR HSSP; P38399; 1JM7.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR Pfam; PF00643; zf-B-box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PROSITE; PS01119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 351 AA; 39723 MW; BF906A21340C4D97 CRC64;

Alignment Scores:
Pred. No.: 2,03e-106 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 2 Gaps: 0

US-10-775-649-5 (1-1597) x Q91Z63 (1-351)

QY 299 ATGGATTATTAATCTAGCTGATCTCTGATGGAACCTATGAGAACCTGGAGAACGAG 358
DB 1 MetAspTyrLysSerGlyLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCTCTGCTGGAGAGTTTACCAAGCCTGTGTATCTGCTGCCCTCCAA 418
DB 21 LeuIleCyProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACCTTCGCGGAAGTGTGCCAACGACATCTTCAGGCTGCGAATCCCTACTGGACC 478
DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGGTGGCTCAGTGTCCATGTCTGGAGTGTCTTCCGTGCCCCCTGCGCCCAT 538
DB 61 AsnArgLysSerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTATCATGACCGCGCAGCGGGGTGACGGCTGCAGAGAACTGCTGGTGGGAAAC 598
DB 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATTCACAGCAGGAGTCTCTCAGTGGCCCCCTGCAGAAAGCAGCCCG 658
DB 101 IleIleAspIleTyrLysGlnGluCysSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGACACAGACGAGAGATCAACATCTACTGTCTCAGTGTGAGTGCCT 718
DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTGCAAGGTGTTGGGGCTCACAGGCTGTGAGGTGCTCCCTTTGCAA 778
DB 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCACAGGACAGAACTAGCTGAGTGAATCTCATCTCCATGTGTGGCGGG 838

DB 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTTCAGACGATCATCTCTAGCTGGAGGACTCTGTCAGAGTACCAGGAG 898
DB 181 AsnAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGTGAAGGAGGAGCTGAGTCAAGAGTTTTCACACCTCTTACGCCATCTG 958
DB 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
QY 959 GATGAGAAGACGAGCTGCTGCAGCGGATCAAGCAGGAGCAGGAGAGCTGGGC 1018
DB 221 AspGluLysLysSerGluLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGln 240
QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGGAGCTGGAAAGTCCACCAAGCTTGTG 1078
DB 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATCCAGTCCCTGGATGAGCCGCGAGGGGCTTACCTCTCTCAAGTGCAG 1138
DB 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAAGCAGCATTCAGAGCCTCAAGGCTGCGAGTGGGGAGACAGACAA 1198
DB 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GGCTTTGAAACATGGACTACTTACTCTGGACTTAGACACATAGCAGAGCCTTGAGG 1258
DB 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
DB 321 AlaIleAspPheGlyThr 326

RESULT 2
Q6NR77 :
ID Q6NR77 PRELIMINARY; PRT; 346 AA.
AC Q6NR77; (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Ring finger protein 28.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Bisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; BF007373; AAP36037.1; -.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR004931; Pro/parathymosin.
DR InterPro; IPR000315; Znf Bbox.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF03247; Prothymosin; 1.
DR Pfam; PF00643; zf-B-box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 346 AA; 39275 MW; F835CA80F7CF53FA CRC64;

Alignment Scores:

Pred. No.:	1.97e-102	Length:	346
Score:	1613.00	Matches:	305
Percent Similarity:	96.95%	Conservative:	13
Best Local Similarity:	92.99%	Mismatches:	10
Query Match:	56.64%	Indels:	0
DB:	2	Gaps:	0
US-10-775-649-5 (1-1597) x QGNR77 (1-346)			
QY	299	ATGGATTATTAATCTAGCTGATCTCTGATGAAACGCTATGAGAACCTGGAGAACGAG	358
DB	1	MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln	20
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCCTGGTCTCATCTGCTGCCCA	418
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40
QY	419	CACACCTCTCCGAGTGTCCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr	60
QY	479	AACCGCGTGGCTCAGTGTCCATGCTGAGGATCGTTTCCGTTGCCCTCGTGGCCGCAAT	538
DB	61	SerArgGlySerSerValSerMetSerGlyArgPheArgCysProThrCysArgHis	80
QY	539	GAAGTATCATGGACCGGACGGGTGTACGCCCTGCAGAGGAACCTGCTGTTGAAAC	598
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100
QY	599	ATCATGTGATCTACAGCAGAGTGTCTCCAGTCCGCGCCCTCAGAAAGGACGACCGG	658
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120
QY	659	ATGTCCAGGAACAGACAGAGAGTCAACATCTACTGTCTCAGCTGTGAGTGCTCT	718
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140
QY	719	ACTTCTCTCTTGTGCAAGTGTGTGGGCTCACAGGCTGTGAGGTGTGCCCTTTGCA	778
DB	141	ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln	160
QY	779	AGCATCTTCCAGGACAGAGTGTGAGTGAATCTGATCTCCATCTGCTGTGGCGGG	838
DB	161	SerValPheGlnGlyLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly	180
QY	839	AACGACGAGTCCAGACGATCATCTCTCAGCTGGAGGACTCTGACAGTGTACCAAGAG	898
DB	181	AsnAspArgValGlnThrIleThrGlnLeuGluAspSerArgArgValThrLysGlu	200
QY	899	AATAGCCACCAAGTGAAGGAGGAGTGTGAGTCAAGAGTTTGACACCTCTACGCCATCCTG	958
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220
QY	959	GATGAGACAGAGGAGTGTGAGTGGAGGATCATCGCAGGACGAGGAGGAGTGGCG	1018
DB	221	AspGluLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLeuSer	240
QY	1019	TTTCATCGGCTCTGATCTCTCAGTACAGGAGGAGTGTGAGGAGTGTGAGGAGTGTG	1078
DB	241	PheIleGluAlaLeuIleGlnGlnThrGlnGlnGlnLysLeuAspSerThrLysLeuVal	260
QY	1079	GAGACCGCCATCCAGTCTGATGAGGCGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTG	1138
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys	280
QY	1139	CAGCTCATCAAGAGCTTTAGAGCTCCAGGCTGCGAGGCTGCGAGGAGGAGGAGGAG	1198
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300
QY	1199	GCCTTTGAAACATGAGTACTTCTCTGAGTGTAGACATAGCAGGAGGAGGAGGAGG	1258
DB	301	GlyPheGluAsnMetAspPheThrThrLeuAspLeuGluHisIleAlaAspAlaLeuArg	320

QY	1259	GCCATTGACTTTGGGACAGGTTAAA	1282
DB	321	AlaIleAspPheGlyAlaAlaGlu	328
RESULT 3			
RN28_HUMAN	STANDARD;	PRT;	353 AA.
ID	RN28_HUMAN	Q96B03; Q96BD9; Q9BYV4;	
AC	Q96B03; Q96BD9; Q9BYV4;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	RING finger protein 28 (Muscle specific ring finger protein 1) (MURF1)		
DE	(Striated muscle RING zinc finger protein) (Iris ring finger protein).		
GN	Name=RNF28; Synonyms=IRF, MURF1, SMR2;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 2).		
RX	MEDLINE=21140140; PubMed=11243782; DOI=10.1006/jmbi.2000.4448;		
RA	Centner T., Yano J., Kimura E., McElhinny A.S., Pelin K., Witt C.C.,		
RA	Bang M.-L., Trombitas K., Granzier H., Gregorio C.C., Sorimachi H.,		
RA	Labat S.;		
RT	"Identification of muscle specific ring finger proteins as potential		
RL	regulators of the titin kinase domain.";		
RL	J. Mol. Biol. 306:717-726(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21316434; PubMed=11283016; DOI=10.1074/jbc.M011208200;		
RA	Dai K.-S., Liew C.-C.;		
RT	"A novel human striated muscle RING zinc finger protein, SMR2,		
RL	interacts with SMT3b via its RING domain.";		
RL	J. Biol. Chem. 276:23992-23999(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE=Iris;		
RA	Wistow G.;		
RT	"IRF: a novel ring finger protein from iris.";		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE=Skeletal muscle;		
RA	Stanchi F.;		
RT	"Characterisation of MURF2, a new muscle-specific RING finger protein		
RL	of the RBCC family that associates with microtubules.";		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE=Skeletal muscle;		
RX	PubMed=14702039; DOI=10.1038/ng1285;		
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,		
RA	Kamakura A., Hayaishi K., Sato H., Nagai K., Kimura K., Makita H.,		
RA	Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,		
RA	Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,		
RA	Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,		
RA	Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,		
RA	Sugawara M., Takahashi M., Kanda K., Yokoi T., Kikkawa E.,		
RA	Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,		
RA	Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,		
RA	Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,		
RA	Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,		
RA	Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,		
RA	Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,		
RA	Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,		
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,		
RA	Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,		
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,		
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,		
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,		
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,		
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y., Okamoto S.,		
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y.,		

RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Sato T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 RP [6].
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- SUBUNIT: Interacts with SM73b and titin.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q969Q1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q969Q1-2; Sequence=VSP_005756;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Muscle specific.
 CC -!- SIMILARITY: Contains 1 B box-type zinc finger.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
 CC frameshift in position 142.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ291713; CAC33173.1; -;
 DR EMBL: AF361946; BAK52497.1; ALT_FRAME.
 DR EMBL: AF353673; BAK39519.1; -;
 DR EMBL: AJ276484; CAB81706.1; -;
 DR EMBL: AK056942; BAB71318.1; -;
 DR EMBL: BC015717; AAH15717.1; -;
 DR HSSP: P38398; 1JM7.
 DR Genew: HGNC:16007; RNF28.
 DR H-InvDB: HIX0000284; -;
 DR MIM: 606131; -;
 DR GO: GO:0005737; C.cytoplasm; NAS.
 DR GO: GO:0005874; C.microtubule; NAS.
 DR GO: GO:0004871; F:signal transducer activity; NAS.
 DR GO: GO:0007165; P:signal transduction; NAS.
 DR InterPro: IPR008938; ARM.
 DR InterPro: IPR000315; Znf_Box.
 DR InterPro: IPR001841; Znf_ring.

DR Pfam: PF00643; zf-B_box; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00336; BBOX; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00119; ZF_BOX; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS00089; ZF_RING_2; 1.
 KW Alternative splicing, Coiled coil, Nuclear protein, Zinc-finger.
 FT ZN_FING 23 79 RING-type.
 FT ZN_FING 117 159 B_box-type.
 FT DOMAIN 207 269 Coiled coil (Potential).
 FT VARSPPLIC 1 13 Missing (in isoform 2).
 FT FTID=VSP_005756.
 FT CONFLICT 237 237 K -> E (in Ref. 1 and 6).
 FT CONFLICT 326 353 TDEEEEFEEEDQEEESTEGKEGHQ -> AAEDDEDDDD
 FT VTIKKQKTDEDD (in Ref. 6).
 SQ SEQUENCE 353 AA; 40247 MW; 9B54B1505039BC86 CRC64;
 Alignment Scores:
 Pred. No.: 1-98e-102 Length: 353
 Score: 1613.00 Matches: 305
 Percent Similarity: 97.55% Conservatives: 13
 Best Local Similarity: 93.56% Mismatches: 8
 Query Match: 56.64% Indels: 0
 DB: 1 Gaps: 0
 US-10-775-649-5 (1-1597) x RN28_HUMAN (1-353)
 QY 299 ATGGATTATTAATCTAGCTGATTCCTGTGGAAGACGTATGAGAACCTGGAGAGCGAG 358
 DB 1 MetAspTyrLysSerSerLeuileGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
 QY 359 CTGATCTGCCCATCTGCTCGAGAGTGTTCACAGCCTGTGTCTATCTGCTGCCCA 418
 DB 21 LeuileCysProileCysLeuGluMetPheThrLysProValileLeuProCysGln 40
 QY 419 CACAACTCTGCGGAAGTGTGCCAACGACATCTTCAGGCTGCGAATCCCTACTCGACC 478
 DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr 60
 QY 479 AACCGGGTGGCTCAGTGTCCATGTCTGAGGTGCTTTCCTGCTGCTGCTGCTGCCCAT 538
 DB 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
 QY 539 GAAGTGATCATGCGCGGCGGCGGTACGCGCTGCAGAGGACCTGCTGTGTGGAAC 598
 DB 81 GluValileMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
 QY 599 ATCATTGACATCTACAAGCAGAGTGCTCCAGTCCGCGCTGCAGAAAGCAGCACCCG 658
 DB 101 IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
 QY 659 ATGTGCAAGGAACACAGAGCAGAGAGATCAACATCTACTGTCTACGTGTGAGTGCT 718
 DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
 QY 719 ACTTCTCTCTCTGCAAGGTGTTGGGCTCACAGGCTGAGGTGCTGCTGCTGCTGCTGCA 778
 DB 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
 QY 779 AGCATCTTCCAAAGGACAGAGACTGAGCTGAGTAACTGCATCTCCATGCTGCTGCTGG 838
 DB 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
 QY 839 AACGACCGAGTGCAGAGATCATCTCTCAGCTGGAGGACTCTGTCAGAGTGAACAGGAG 898
 DB 181 AsnAspArgValGlnThrIleThrGlnLeuGluAspSerArgArgValThrLysGlu 200
 QY 899 AATAGCCACCGGTGAAGGAGGAGCTGAGTACAGAGTTTGACACCTCTACGCCATCTCG 958
 DB 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220
 QY 959 GATGAGAAGAAGCGAGCTGCTGCAGCGGATTCACGACGAGGACGAGGAGGAGCTGGGC 1018


```
QY 899 AATAGCCACCAGCTGAGGAGGAGCTGAGTCAGACAGTTTGACACCCCTTACGCCATCTTG 958
Db 198 AenSerLysSerLysLysGluHisValAsnGluMetPheGluThrLeuSerArgCysLeu 217
QY 959 GATGAGAAGAGCAGGAGCTGTCGACGGATCACCCAGAGCAGGAGGAGGAGGAGGAGGAG 1018
Db 218 GluGluLysLysThrHisLeuValGlnGlnIleSerGlnAlaGluGluGluLysLeuAsn 237
QY 1019 TTCATCGAGGCTGATCTCTCCAGTACAGGGAGCAGCTGGAAAGTCCACCAAGCTTGTG 1078
Db 238 IleValArgSerLeuIleValArgCysGlnGlnLeuGlnSerSerAsnGluLeu 257
QY 1079 GAGACCGCCATCCAGTCCCTGATGAGCCGAGGGGCTACCTTCTCTCAAGTGCACAG 1138
Db 258 GlnAsnAlaPheGlnAlaMetGluGlnThrGlyProAlaAsnPheLeuLeuGluSerLys 277
QY 1139 CAGCTCATCAAGAGCATTTAGAACCTCAAGGGCTGCAGCTGGGGAGACAGAGCAA 1198
Db 278 GlnLeuIleLysLysLeuMetGluAlaSerLysGlyCysGlnLeuGluLysThrGluLeu 297
QY 1199 GCGTTTGAGAACATGACTTACTCTGGACTTAGACATAGCAGGAGGCTTGAGG 1258
Db 298 GlyPheGluAsnMetAspGlnPheThrLeuAspMetGluHisValSerGlnCysLeuArg 317
QY 1259 GCCATTGACTTTGGGACAGGTAAAGGATGATGAT 1291
Db 318 AsnIleAspPheSerAla-----AsnCysAsp 326

RESULT 5
ID Q81UD9 PRELIMINARY; PRT; 540 AA.
AC Q81UD9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RING finger protein 29.
GN Name=RNF29;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Iakovenko A., Gautel M.;
RT "Titin-associated zinc-finger proteins link titin kinase to
RL J. Muscle Res. Cell Motil. 21:833-833 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=22302063; PubMed=12414993;
RA Flizon V., Iakovenko A., Van der Ven P.F.M., Kelly R.A., Fatu C.,
RA Furst D.O., Karsenti E., Gautel M.;
RT "Transient association of titin and myosin with microtubules in
RT nascent myofibrils directed by the MURF2 RING-finger protein.";
RL J. Cell Sci. 115:4469-4482 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Gautel M.S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AJ431704; CAD24432.1;
DR GO; GO:0000151; Cubititin ligase complex; IEA.
DR GO; GO:0004842; F-ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F-zinc ion binding; IEA.
DR GO; GO:0016567; P-protein ubiquitination; IEA.
DR InterPro; IPR000315; Znf-Bbox.
DR InterPro; IPR001841; Znf-ring.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
```

```
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00899; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 540 AA; 60245 MW; D16B7E06BF9C60A CRC64;

Alignment Scores:
Pred. No.: 6,43e-69 Length: 540
Score: 1126.50 Matches: 221
Percent Similarity: 67.00% Conservative: 45
Best Local Similarity: 55.67% Mismatches: 60
Query Match: 39.55% Indels: 71
Db: 2 Gaps: 2

US-10-775-649-5 (1-1597) x Q81UD9 (1-540)
QY 80 ATGAGCAGCTTCTCTGAATTACAAGTCTTTCTTCCAAAGAGCAGACCATGGATACTTG 139
Db 1 MetSerAlaSerLeuAsnTyrlsSerPheSerLysGluGlnThrMetAsp----- 18
QY 140 GAAAAGCAACTGATCTGTCCTCCATCTCGCTAGAGATGTTCCAGAACCTGTGTCTCTC 199
Db 18 ----- 18
QY 200 CCTTGCACGACACACCTGTGCAGGAAATGTGCGGGCCCCCTTGGAGACAAAGACTTGT 259
Db 18 ----- 18
QY 260 GTGACGAGGTGGGCAAGACAGTCGCATTTCAAAGCAATATGGATTATAAATCTAGCCTG 319
Db 18 ----- 18
QY 320 ATTCTGATGGAACGCTATGGAGAACCTGGAGAGACAGCTGATCTGCCCATCTGCTCG 379
Db 19 -----AsnLeuGluLysGlnLeuIleCysProIleCysLeu 30
QY 380 GAGATGTTTACCAAGCTGTGTGTCATCTGCCCTTCCAAACACACACCTCTGCCGGAAGTG 439
Db 31 GluMetPheThrLysProValValIleLeuProCysGlnHisAsnLeuCysArgLysCys 50
QY 440 GCCAACGACATCTTCCAGGCTCGGAATCCTACTCGACCAACCGCGGTGGCTCAGTGTCC 499
Db 51 AlaSerAspIlePheGlnAlaSerAsnProTyrLeuProThrArgGlyGlyThrThrMet 70
QY 500 ATGCTCTGAGGTGCTTTCCGTTGCCCTCGTCCGCCCATGAAGTATCATGACCGCCGAC 559
Db 71 AlaSerGlyGlyArgPheArgCysProSerCysArgHisGluValValLeuAspArgHis 90
QY 560 GGGGTGTACGGCTGCAGAGGAACCTGTGTGGTGGAAACATCATTTACATCTACAAGCAG 619
Db 91 GlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsnIleLeuAspIleTyrLysGln 110
QY 620 GAGTGTCTCAGTCGGCCCTCGCAGAAAGCAGCACCCTGATGTGCAAGAAACACGAAAGAC 679
Db 111 Glu---SerThrArgProGluLysLysSerAspGlnProMetCysGluGluHisGluGlu 129
QY 680 GAGAGATCAACATCTACTCTCTCAGTGTGAGGTGCTTCTGCTCTCTGTCAGAGGTG 739
Db 130 GluArgIleAsnIleTyrCysLeuAsnCysGluValProThrCysSerLeuCysLysVal 149
QY 740 TTTGGGGCTCACGAGGCTGTGAGGTGCGCCCTTTGCAAAAGCATCTTCCAAGGACAGAAG 799
Db 150 PheGlyAlaHisLysAspCysGlnValAlaProLeuThrHisValPheGlnArgGlnLys 169
QY 800 ACTGAGCTGAGTAATCTCATCTCCATGCTGTGGTGGGGGAAACGACCGATGTCAGAGATC 859
Db 170 SerGluLeuSerAspGlyIleAlaIleLeuValGlySerAsnAspArgValGlnGlyVal 189
QY 860 ATCTCTCAGCTGGAGGCTCGTGCAGATGACCAAGGAGAATAGCCACGAGGTGAGGAG 919
Db 190 IleSerGlnLeuGluAspThrCysLysThrIleGluGluCysCysArgLysGlnLysGln 209
```

QY 920 GAGCTGAGTCAAGTTTGGACCCCTCTACGCCATCTGATGAGAAGAGCGAGCTG 979
 DB 210 GluLeuCyGluGlyPheAspTyrLeuTyrGlyLeuGluGluArgLysAsnGluMet 229
 QY 980 CTGACGGGATCAGCAGGAGGAGGAGGAGCTGGCTTCATCGAGCTCTGATCCTC 1039
 DB 230 ThrGlnValIleThrArgThrGlnGluGluLysLeuGluHisValArgAlaLeuLys 249
 QY 1040 CAGTACAGGAGCAGCTGGAAGAAGTCCACCAAGCTTGTGGAGACGCCATCCAGTCCCTG 1099
 DB 250 LysTyrSerAspHisLeuGluAsnValSerLysLeuValGluSerGlyIleGlnPheMet 269
 QY 1100 GATGACCCGGAGGGGCTACCTCTCTCAAGTGCACAGCAGCTCATCAAGAGCTGTA 1159
 DB 270 AspGluProGluMetAlaValPheLeuGluAsnAlaLysThrLeuLysLysIleSer 289
 QY 1160 GAAGCTCCAGGGCTGCCAGCTGGGAGAGCAGAGCAGGCTTGTGAGACATGACTAC 1219
 DB 290 GluAlaSerLysAlaPheGlnMetGluLysIleGluHisGlyTyrGluAsnMetAsnHis 309
 QY 1220 TTACTCTGAGCTTAGAACACATAGCAGAGGCTTGGAGGCCATGACTTT 1270
 DB 310 PheThrValAsnLeuAsnArgGluGluLysIleIleArgGluIleAspPhe 326

RESULT 6
 Q6INV6
 ID Q6INV6 PRELIMINARY; PRT; 360 AA.
 AC Q6INV6;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE MGC80214 protein.
 GN Name=MGC80214;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]

SEQUENCE FROM N.A.
 TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC 1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL; BC072166; AA072166.1; 1.
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR000315; Znf Bbox.
 DR InterPro; IPR001841; Znf Bbox.
 DR Pfam; PF00643; ZF-B_box; 1.
 DR Pfam; PF00097; ZF-C3HC4; 1.
 DR SMART; SM00336; BBOX; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00119; ZF_BBOX; 1.
 DR PROSITE; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 360 AA; 40971 MW; 35B5D6E162C1E5CD CRC64;
 Alignment Scores:
 Pred. No.: 1,49e-68 Length: 360
 Score: 1120.50 Matches: 208
 Percent Similarity: 82.35% Conservative: 58
 Best Local Similarity: 64.40% Mismatches: 54
 Query Match: 39.34% Indels: 3
 DB: 2 Gaps: 2
 US-10-775-649-5 (1-1597) x Q6INV6 (1-360)
 QY 317 CTGATTCCTGATGGAACCGCTATGGAGAACCTGGAGAACGAGCTGATCTGCCCATCTGC 376
 DB 10 LeuAlaGlyAspThrGlnThrMetAspAsnLeuGluLysGlnLeuLeuCysProIleCys 29
 QY 377 CTGGAGATGTTTACCAAGCCCTGTGCTCATCTGCTCCCTGCCAACACAACTCTGCCGGAAG 436
 DB 30 LeuGluMetPheThrLysProValIleLeuProCysGlnHisAsnLeuLysArgLys 49
 QY 437 TGTGCCAAGCATCTTCCAGGCTCCGAGCTCCCTACTCCCTACCGAACCAACCGGGTGGCTCAGTG 496
 DB 50 CysAlaAsnAspIlePheGlnAlaSerAsnProLeuTrpGlnSerArgGlySerThr 69
 QY 497 TCCATGCTCGAGGTCGTTTCGTTGCCCTCGTCCGCGCATGAAGTATCATGACACCGG 556
 DB 70 ValSerSerGlyArgPheArgCysProSerCysArgHisGluValValLeuAspArg 89
 QY 557 CACGGGGTGTACGGCTCCAGAGGAACCTGTGTGGTGGAAACATCATTCATCATCAAG 616
 DB 90 HisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsnIleIleAspIleTyrLys 109
 QY 617 CAGGAGTCTCCAGTCCGCGCTCCGAGAGGAGCAGC-----CACCCGATGTCAAGGA 670
 DB 110 GlnGlu---SerSerArgProMetAsnProLysSerGluGlnHisLeuMetCysGluGlu 128
 QY 671 CACGAAGACGAGAAGATCAACATCTACTCTCAGCTGTGAGGTGCTACTTGTCTCTTG 730
 DB 129 HisGluAspGluLysIleAsnIleTyrCysLeuSerCysGluValProThrCysSerMet 148
 QY 731 TGCAAGGTGTTGGGGCTCACACAGGCTGTGAGGTGGCCCTTTGCAAGCATCTTCAA 790
 DB 149 CysLysValPheGlyAlaHisLysAspCysGluValAlaProLeuSerSerIleTyrLys 168
 QY 791 GGACAGAAGACTGAGCTGAGTAACTGCATCTCCATCTGCTGGTGGCGGGACACCGAGTG 850
 DB 169 ArgGlnLysSerGluLeuSerAspGlyIleAlaMetLeuValGlyGlyAsnAspArgIle 188
 QY 851 CAGAGCATCATCTCTCAGCTGGAGGACTCTGTGTCAGGTGACCAAGGAGAATAGCCACCAAG 910
 DB 189 GlnAlaValIleThrGlnIleGluLysSerIleGluAspAsnSerArgArg 208
 QY 911 GTGAAGGAGGAGCTGAGTCAGAAAGTTTGCACACCTCTACGCCATCTCGATGAGAAGAG 970

Db	209	GlnLysGlnLeuLeuSerGlnArgPheAspSerLeuTyrAsnIleLeuGluGluArgLys	228
Qy	971	AGCGAGCTGCTGCAGCGGATCACCGCAGGACGAGGAGAGCTGGGCTTCATCGAGGCT	1030
Db	229	LysGluLeuLeuGlnMetValThrArgGlnGlnGluGluLysLeuGlnCysValArgGly	248
Qy	1031	CTGATCTCCAGTACACGAGGAGAGCTGGAAAAGTCCACCAAGCTTGTTGGAGACGCCATC	1090
Db	249	LeuIleArgGlnHisGlyAspHisLeuGluValThrSerLysLeuValGluSerSerIle	268
Qy	1091	CAGTCCCTGATGATGCGCGGAGGGCTACTCTCTCAAGTCCAGAGAGCTCATCAAG	1150
Db	269	GlnSerMetGluGluProGlnMetAlaAlaPheLeuGlnAsnAlaLysGluLeuIleLys	288
Qy	1151	AGCATTTGTAGAAGCCTCCAAGGGCTGCAGCTGGGGAAGACAGACGAAGGCTTTGAGAAC	1210
Db	289	LysIleSerAspMetSerLysValSerThrIleGluArgProGluProGlyTyrGluAsn	308
Qy	1211	ATGAGCTACTTTTACTCTGGACTTAGAACACATAGCAGAGCGCTTGAGGGCCATTGACTTT	1270
Db	309	MetGluHisPheSerValAsnValAspTyrValSerGluMetLeuArgThrIleAspPhe	328
Qy	1271	GGGACAGCT	1279
Db	329	HisSerGly	331
RESULT 7			
Q96DV3 PRELIMINARY; PRT; 452 AA.			
ID	Q96DV3	PRELIMINARY;	PRT; 452 AA.
AC	Q96DV3;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	RING finger protein 29.		
GN	Name=RNFP29;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Cardiac muscle;		
RA	Iakovenko A., Gautel M.;		
RT	"Titin-associated zinc-finger proteins link titin kinase to		
RT	transcriptional control.";		
RL	J. Muscle Res. Cell Motil. 21:833-833 (2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Cardiac muscle;		
RX	MEDLINE=22302063; PubMed=12414993;		
RA	Pizon V., Iakovenko A., Van der Ven P.F.M., Kelly R.A., Fatu C.,		
RA	Furst D.O., Karasenti E., Gautel M.;		
RT	"Transient association of titin and myosin with microtubules in		
RT	nascent myofibrils directed by the MURF2 RING-finger protein.";		
RL	J. Cell Sci. 115:4469-4482 (2002).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Cardiac muscle;		
RA	Gautel M.S.;		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: Contains 1 RING-type zinc finger.		
DR	EMBL: AJ243488; CAC43019.1;		
DR	GO: GO:0000151; C-ubiquitin ligase complex; IEA.		
DR	GO: GO:0004842; F-ubiquitin-protein ligase activity; IEA.		
DR	GO: GO:0008270; F-zinc ion binding; IEA.		
DR	GO: GO:0016567; P:protein ubiquitination; IEA.		
DR	InterPro: IPR000315; Znf Bbox.		
DR	InterPro: IPR001841; Znf_Ring.		
DR	Pfam: PF00643; zf-B_box; 1.		
DR	Pfam: PF00097; zf-C3HC4; 1.		
DR	SMART: SM00336; BBOX; 1.		
DR	SMART: SM00184; RING; 1.		

```

Db      210  GluLeuCysGluPheAspTyrLeuTyrGlyIleLeuGluGluArgLysAsnGluMet 229
Qy      980  CTGACGGGATCACCGAGCAGGAGAGAGCTGGGCTTCATCGAGCTCTGATCCTC 1039
Db      230  ThrGlnValIleThrGlnGluGluGluGluHisValArgAlaLeuIleLys 249
Qy      1040  CAGTACAGGAGCAGCTCGAAAGTCCACCAAGCTGTGGAGACCGCCATCCAGTCCCTG 1099
Db      250  LysTyrSerAspHisGluGluAsnValSerLysLeuValGluSerGlyIleGlnPheMet 269
Qy      1100  GATGAGCGGAGGGCTACCTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATTGTA 1159
Db      270  AspGluProGluMetAlaValPheLeuGlnAsnAlaLysThrLeuLeuLysIleSer 289
Qy      1160  GAAGCTCCAGGGCTCGCAGCTGGGAGAGCAGCAAGGCTTTGAGAACATGAGCTAC 1219
Db      290  GluAlaSerLysAlaPheGlnMetGluLysIleGluHisGlyTyrGluAsnMetAsnHis 309
Qy      1220  TTTACTCTGGACTTAGAACACATAGCAGAGGCTTTGAGGGCCATTGACTTT 1270
Db      310  PheThrValAsnLeuAsnArgGluGluLysIleIleArgGluIleAspPhe 326

RESULT 8
Q96DV2 PRELIMINARY; PRT; 548 AA.
AC Q96DV2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE RING finger protein 29.
GN Name=RNFP29;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Cardiac muscle;
RA Iakovenko A., Gautel M.;
RT "Titin-associated zinc-finger proteins link titin kinase to
transcriptional control.";
RL J. Muscle Res. Cell Motil. 21:833-833 (2000).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Cardiac muscle;
RA Pizon V., Iakovenko A., Van der Ven P.F.M., Kelly R.A., Fatu C.,
Furt D.O., Karsenti E., Gautel M.;
RT "Transient association of titin and myosin with microtubules in
nascent myofibrils directed by the MURF2 RING-finger protein.";
RL J. Cell Sci. 115:4469-4482(2002).
RN [3]
SEQUENCE FROM N.A.
RP TISSUE=Cardiac muscle;
RA Gautel M.S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AJ243489; CAC43020.1; -
DR GO; GO:0000151; Cribinutin ligase complex; IEA.
DR GO; GO:0004842; Fubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR000315; Znf Bbox.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00518; ZF_RING_2; 1.
DR PROSITE; PS00518; ZF_RING_3; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW

```

```

SQ SEQUENCE 548 AA; 60465 MW; D7AB530A359FD67D CRC64;
Alignment Scores:
Pred. No.: 1.96e-68 Length: 548
Score: 1119.50 Matches: 220
Percent Similarity: 66.75% Conservative: 45
Best Local Similarity: 55.42% Mismatches: 61
Query Match: 39.31% Indels: 71
DB: 2 Gaps: 2
US-10-775-649-5 (1-1597) x Q96DV2 (1-548)
Qy 80 ATGAGCACTTCTGGAATTACAGTCTTCTCCAAAGAGCAGCAGCAGTGAATCTTG 139
Db 1 MetSerAlaSerLeuAsnTyrLysSerPheSerLysGluGlnGlnThrMetAsp 18
Qy 140 GAAAAGCAACTGATCTGTCCCATCTGCTAGAGATGTTTCAAGAGCCTGTGCTC 199
Db 18 ----- 18
Qy 200 CTTGTCAGCACAACCTGTGAGGAAATGTGGGGCCCCCTTGGAGAGCAAGACTGT 259
Db 18 ----- 18
Qy 260 GTGACGCGAGGTGGGCAACAGCAGTCGCATTTCAAGCAATATGGATTATAATCT 319
Db 18 ----- 18
Qy 320 ATTCTGTATGGAACCGCTATGGAGAACCTGGAGAACCTGGAGAGCAGCTGATCTG 379
Db 19 -----AsnLeuGluLysGlnLeuIleCysProIleCysLeu 30
Qy 380 GAGATGTTTACCAAGCCTGTGTCTCATCTGCTGCCCTGCCAACACAACTCTGCGG 439
Db 31 GluMetPheThrLysProValIleLeuProCysGlnHisAsnLeuCysArgLysCys 50
Qy 440 GCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGAACCAACCGGCTGCTCAG 499
Db 51 AlaSerAspIlePheGlnAlaSerAsnProTyrLeuProThrArgGlyIleThrMet 70
Qy 500 ATGCTGGAGTCTGTTCCGCTGCTGCCCTGCTGCCCTGCTGCTGCTGCTGCTGCTG 559
Db 71 AlaSerGlyLysArgPheArgCysProSerCysArgHisGluValIleLeuAspArgHis 90
Qy 560 GGGGTGTACGGCTGCAGAGGAACCTGCTGTGTGGAAAAACATCATTCATCTACAAG 619
Db 91 GlyValTyrGlyLeuGlnArgAsnLeuValGlyAsnIleAspIleTyrLysGln 110
Qy 620 GAGTCTCCAGTCCGCGCCCTCGAGAAAGGCGACCCAGTGTGCAAGAACACAGAGAC 679
Db 111 Glu---SerThrArgProGluLysLysSerAspGlnProMetCysGluGluHisGlu 129
Qy 680 GAGAGATCAACATCTACTGTCTCAGCTGAGGTGCTTCTCTCTCTCTCTCTCTCTCT 739
Db 130 GluArgIleAsnIleTyrCysLeuAsnCysGluValProThrCysSerLeuCysVal 149
Qy 740 TTTGGGCTCCACGCGCTGTGAGTTCCTCCCTTTGCAAGCATCTTCCAAAGCAGAG 799
Db 150 PheGlyAlaHisLysAspCysGlnValAlaProLeuThrHisValPheGlnArgGlnLys 169
Qy 800 ACTGAGCTGAGTAAGTCAATCTTCATGCTGTGGTGGCGGGAGCAAGCAGTGTGAG 859
Db 170 SerGluLeuSerAspGlyIleAlaIleValGlySerAsnAspArgValGlnGlyVal 189
Qy 860 ATCTCTCAGCTGAGGAGCTCGTGCAGAGTGCACCAAGAGAAATAGCCACAGTGA 919
Db 190 IleSerGlnLeuGluAspThrCysLysThrIleGluGluCysCysArgLysGlnLysGln 209
Qy 920 GAGCTGTAGTCAAGATTTTGACACCCCTCTACGCGCATCTCTGGATGAGAAGAGC 979
Db 210 GluLeuCysGluLysPheAspTyrLeuTyrGlyIleLeuGluGluArgLysAsnGluMet 229
Qy 980 CTGCAGCGGATCACCGAGGAGGAGAGCTGGGCTTCATCGAGGCTCTGATCTCTC 1039

```

Db 230 ThrGlnValIleThrArgThrGlnGluGluLysLeuGluHisValArgAlaLeuIleLys 249
QY 1040 CAGTACAGGAGCAGCTGGAAAGTCCACCAGCTTGTGGAGACCCCATCCAGTCCCTG 1099
Db 250 LysTyrSerAspHisLeuGluAsnValSerLysLeuValGluSerGlyIleGlnPheMet 269
QY 1100 GATGACCCGGAGGGCTACCTCTCAAGTGCCCAAGCAGCTCATCAAGACATTGTA 1159
Db 270 AspGluProGluMetAlaValPheLeuGlnAsnAlaLysThrLeuLeuLysIleSer 289
QY 1160 GAAGCTCCAGGCTGCCAGCTGGGAGACAGACAAGCGCTTTCAGAACATGGACTAC 1219
Db 290 GluAlaSerLysAlaPheGlnMetGluLysIleGluHisGlyTyrGluAsnMetAsnHis 309
QY 1220 TTTACTCTGGACTTAGAACACATAGCAGAGCGCTTGGAGCCCATTCATT 1270
Db 310 PheThrValAsnLeuAsnArgGluGluLysIleAlaArgGluIleAspPhe 326

RESULT 9
Q9ERP3 PRELIMINARY; PRT; 366 AA.
AC Q9ERP3; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RING-finger protein MURF.
GN Name=Rnf30;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP "Regulation of microtubule dynamics and myogenic differentiation by
RT MURF, a striated muscle RING-finger protein.";
RL J. Cell Biol. 150:771-784 (2000).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF294779; AAC03076.1; -
DR MGD; MGI:189623; Rnf30.
DR GO; GO:0005875; C: microtubule associated complex; IDA.
DR GO; GO:0008017; F: microtubule binding; IDA.
DR GO; GO:0007026; P: microtubule stabilization; IDA.
DR InterPro; IPR00315; Znf Bbox.
DR InterPro; IPR001841; Znf ring.
DR Pfam; PF00643; zf-B box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00119; ZF BBOX; 1.
DR PROSITE; PS00518; ZF RING 1; 1.
DR PROSITE; PS00089; ZF RING 2; 1.
KW Metal-binding; zinc; Zinc-finger.
SQ SEQUENCE 366 AA; 41130 MW; 6CD3429162D5BEFA CRC64;

Alignment Scores:
Pred. No.: 7.9e-68 Length: 366
Score: 1110.00 Matches: 212
Percent Similarity: 78.53% Conservative: 55
Best Local Similarity: 62.35% Mismatches: 63
Query Match: 38.97% Indels: 10
DB: 2 Gaps: 3

US-10-775-649-5 (1-1597) x Q9ERP3 (1-366)

QY 278 ACAGTCGCATTTCAAGACATATGGATTATTAATCTAGCTGATTCCTCATGGAACGCT 337
Db 4 ThrValGlyPheLys-----ProLeuLeuGlyAspAlaHisAsn 16

QY 338 ATGGAGAACCTGGAGAACGAGCTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCT 397
Db 17 MetAspAsnLeuGluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysPro 36
QY 398 GTGGTCATCTCCTGCTGCCAACAACACTCTCTGCCGGAAGTGTGCCAACACATCTTCCAG 457
Db 37 ValValIleLeuProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGln 56
QY 458 GCTGGCAATCCCTACTTGGACCAACCGCGTGCTCAGTCTCCATGCTCTCGAGTCTGCTTC 517
Db 57 AlaSerAsnProLeuIleThrValSerSerGlyGlyArgPhe 76
QY 518 CTTGTCCTCTGCTGCCCATCAAGTATCATCGACCGCGCTGTACGCGCTGCAG 577
Db 77 ArgCysProSerCysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGln 96
QY 578 AGAACCTCTCTGGTGGAAAAACATCATTTGACATCTACAGCAGAGTGTCCAGTCTGGCCCC 637
Db 97 ArgAsnLeuValGluAsnIleAspIleTyrLysGlnGlu---SerSerArgPro 115
QY 638 CTG-----CAGAAAGGCGACCCCGATGTCAGGACACGACGACGAGAGATCAAC 691
Db 116 LeuHisAlaLysAlaGluGlnHisLeuMetCysGluGluHisGluAspGlnLysIleAsn 135
QY 692 ATCTACTGTCTCACGTGTGAGGTGCTCTACTTGTCTGTGCAAGGTGTTTGGGGCTCAC 751
Db 136 IleTyrCysLeuSerCysGluValProThrCysSerLeuCysLysValPheGlyAlaHis 155
QY 752 CAGGCTGTGAGGTGCTCCCTTTGCAAGCATCTTCCAAAGGACAGAACTGAGCTGAGT 811
Db 156 LysAspCysGluValAlaProLeuProThrIleTyrLysArgGlnLysSerGluLeuSer 175
QY 812 AACTGCATCTCCATGCTGTGGCGGAGACCGAGTGCAGACGATCATCTCTCAGCTG 871
Db 176 AspGlyIleAlaMetLeuValAlaGlyAsnAspArgValGlnAlaValIleThrGlnMet 195
QY 872 GAGGACTCTGCAGAGTGCACCAAGGAGATACCCACAGGTGAAGGAGGAGCTGAGTCA 931
Db 196 GluGluValCysGlnThrIleGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGln 215
QY 932 AAGTTTGACACCTCTACGCCATCTCGATGATGAGAGAGAGGAGCTGTGACGCGGATC 991
Db 216 ArgPheGluThrLeuCysAlaValLeuGluGluArgLysGlyGluLeuGlnAlaLeu 235
QY 992 ACGCAGGACGACGAGGAGAGCTGGGCTTCATCAGGCTCTGATCTCCAGTACAGGGAG 1051
Db 236 AlaArgGluGlnGluLysLeuGlnArgValArgGlyLeuIleArgGlnTyrGlyAsp 255
QY 1052 CAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCTCGATGAGCCCGGA 1111
Db 256 HisLeuGluGlySerSerLysLeuValGluSerAlaIleGlnSerMetGluGluProGln 275
QY 1112 GGGGTACCTCTCTCAAGTCCCAAGCAGCTCATCAAGAGCATTTAGAACCTTCAAG 1171
Db 276 MetAlaLeuTyrLeuGlnGlnAlaLysGluLeuIleAsnLysValGlyAlaMetSerLys 295
QY 1172 GGTGCGCAGCTCGGAAAGACAGCAAGCGCTTGTGAAACATGACTACTTTACTCTGGAC 1231
Db 296 ValGluLeuAlaGlyArgProGluProGlyTyrGluSerMetGluGlnPheSerValSer 315
QY 1232 TTAGAACACATAGCAGAGCGCTTGGAGGCGCATTTGGGACAGGTAAAGSAGTGTGAT 1291
Db 316 ValGluHisValAlaGluMetLeuArgThrIleAspPheGlnProGlyAlaAlaGlyAsp 335
RESULT 10
RN29 HUMAN
ID RN29 HUMAN STANDARD; PRT; 436 AA.
AC Q9BYT6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE RING finger protein 29 (Muscle specific ring finger protein 2)
DE (MURF2).

[illegible]

Db 61 ArgCysProSerCysArgHisGluValValLeuAspArgHisGlyValTyrglyLeuGln 80
 QY 578 AGCAACCTCTGCTGGAACACATCATATACAGCAGAGTCTCCAGTCGGCCC 637
 Db 81 ArgAsnLeuValGluAsnIleIleAspIleTyrglyGlnGlu---SerSerArgPro 99
 QY 638 CTGCAGAGGAGCAGC-----CACCCGATGTGCAAGCAACACGAGAGATCAAC 691
 Db 100 LeuHisSerLysalaGluGlnHisLeuMetCysGluGluHisGluGluLysIleAsn 119
 QY 692 ATCTACTGCTCAGGTGAGTGCCTACTGCTCTTGTGCAAGGTGTTGGGCTCAC 751
 Db 120 IleTyrcysLeuSerCysGluValProThrCysSerLeuCysLysValPheGlyAlaHis 139
 QY 752 CAGGCTGTGAGTGTGCGCTTTCACAGCATCTTCCAGGACAGAG----- 799
 Db 140 LysAspCysGluValAlaProLeuProThrIleTyrglyArgGlnLysLysGlnAspLeu 159
 QY 799 ----- 799
 Db 160 ThrLeuLeuProArgLeuGluCysSerGlyThrAsnThrThrTyrcysSerLeuAspLeu 179
 QY 800 -----ACTGAG 805
 Db 180 ProSerSerSerAspProIleLeuAlaSerGlnAsnThrLysIleIleAspSerGlu 199
 QY 806 CTGAGTAACGTGATCTCCATGCTGTCGGCGGAGACGAGTGCAGACGATCATCT 865
 Db 200 LeuSerAspGlyIleAlaMetLeuValAlaGlyAsnAspArgValGlnAlaValIleThr 219
 QY 866 CAGCTCGAGGACTCGTGCAGAGTGACCAAGGAGATAGCCAGGTGAGGAGAGCTG 925
 Db 220 GlnMetGluGluValCysGlnThrIleGluAspAsnSerArgGlnLysGlnLeuLeu 239
 QY 926 AGTCAGAAGTTGACCTCTACGCTGATCTGATGAGAGAGAGAGAGAGTGTGAG 985
 Db 240 ThrGlnArgPheGluSerLeuCysAlaValLeuGluGluArgLysGlyGluLeuLeuGln 259
 QY 986 CGGATCACCGAGGAGGAGGAGAGCTGGGCTTCATCGAGCTCTGATCTCCAGTAC 1045
 Db 260 AlaLeuAlaArgGluGlnGluGluLysLeuGlnAlaValArgGlyLeuLeuArgGlnTy 279
 QY 1046 AGGAGCAGCTGGAAGTCCACCAAGCTGTGAGACCGCCATCCAGTCCCTGATGAG 1105
 Db 280 GlyAspHisLeuAlaSerSerLysLeuValGluSerAlaIleGlnSerMetGluGlu 299
 QY 1106 CCGGAGGGGCTACCTCTCTCAAGTGCAGACGCTCATCAAGAGCATTTGAGAGCC 1165
 Db 300 ProGlnMetAlaLeuTyrglyLeuGlnGlnAlaLysGluLeuIleAsnLysValGlyAlaMet 319
 QY 1166 TCCAGGGGCTGCCAGCTGGGAGAGACAGCAAGGCTTTGAGAACATGACTTTACT 1225
 Db 320 SerLysValGluLeuAlaGlyArgProGluProGlyTyrglySerMetGluGlnPheThr 339
 QY 1226 CTGGACTTAGAACACATAGCAGAGGCTTTGAGGCCATTGACTTTGGGACAGT 1279
 Db 340 ValArgValGluHisValAlaGluMetLeuArgThrIleAspPheGlnProGly 357
 RESULT 14
 Q6DHSO
 ID Q6DHSO PRELIMINARY; PRT; 443 AA.
 AC Q6DHSO;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Zgc:92123.
 GN Names:zgc:92123;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RL -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC GO: GO:000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0004842; P:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; P:zinc ion binding; IEA.
 DR GO: GO:001567; P:protein ubiquitination; IEA.
 DR InterPro: IPR000315; Znf Bbox.
 DR Pfam: PF00643; zf-B box; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART; SM00336; BBOX; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00119; ZF_BBOX; 1.
 DR PROSITE; PS00158; ZF_RING_1; 1.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 KW SEQUENCE 443 AA; 49707 MW; 91324DA47EF083ED CRC64;
 Alignment Scores:
 Pred. No.: 9,448-63 Length: 443
 Score: 1036.50 Matches: 196
 Percent Similarity: 75.84% Conservative: 52
 Best Local Similarity: 59.94% Mismatches: 74
 Query Match: 36.39% Indels: 5
 DB: 2 Gaps: 2
 US-10-775-649-5 (1-1597) x Q6DHSO (1-443)
 QY 299 ATGGATTATAATCTAGCTGATTCCTGATGGAACGCTATCGAGAACCTGGAGAGCAG 358
 Db 5 LeuAspTyrcysLeuSerArgSerArgAsp-----ThrMetGluSerLeuGluArgGln 22
 QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCTGTGTCTCATCTCGCTCCCAA 418
 Db 23 LeuIleCysProIleCysLeuGluIlePheThrLysProValIleLeuProCysGln 42
 QY 419 CACACCTCTGCGGAGAGTGTCCCAACGACATCTCCAGGCTCGGATCCCTACTGACC 478
 Db 43 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaSerAsnProTyrglyLeuPro 62
 QY 479 AACCCGGTGGCTCAGTGTCCATGTCTGAGGTCTGTTCCGTTGCTGCTGCTGCTGCTG 538
 Db 63 ThrArgglyLysSerLeuGlySerGlyGlyArgPheArgCysProSerCysArgHis 82

Result No.	Score	Query Match	Length	DB	ID	Description
1	1802	63.3	343	4	US-09-908-988B-6	Sequence 6
2	1613	56.6	353	4	US-09-484-970B-171	Sequence 1
3	1114.5	39.1	545	4	US-09-908-988B-4	Sequence 4
4	1110	39.0	366	4	US-09-908-988B-2	Sequence 2
5	267.5	9.4	223	4	US-09-327-983-5	Sequence 5
6	257	9.0	435	4	US-09-561-989-10	Sequence 1
7	240	8.4	519	4	US-09-949-016-7883	Sequence 7
8	237	8.3	513	4	US-09-949-016-10972	Sequence 1
9	232.5	8.2	327	4	US-09-949-016-7575	Sequence 7
10	223	7.8	842	4	US-09-949-016-7012	Sequence 7
11	223	7.8	870	4	US-09-949-016-9625	Sequence 9
12	221	7.8	413	4	US-09-663-600A-198	Sequence 1

```
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGCTCATCTGCCCTGCCAA 418
Db 21 LeuileCysProileCysLeuGluMetPheThrLysProValValleLeuProCysGln 40
QY 419 CACAACTCTGCCGAAGTGTGCCACGACATCTTCAGGCTGCGAATCCCTACTGAGCC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGGGTGGCTCAGTCCATGCTCGAGGTCGTTTCCGTGCGCCCTGCGCCGCT 538
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTCATGATGACCGACCGGCGGTGTACGGCTGCAGAGGAACCTGTGTGGAAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAGGAGGAGTCTCCAGTCGGCCCTCGAGAAAGCCACCCG 658
Db 101 IleleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGACACGACGAGATCAACATCTACTGTCTCAGCTGTGAGTGCCT 718
Db 121 MetCysLeuGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTGTGCAAGGTGTTTGGGGCTCACCGGCTGTGAGGTGCGCCCTTGCAA 778
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAAAGGACAGAGCTGAGTGAAGTAACTGCAATCTCCATGCTGTGGCGGG 838
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGAG 898
Db 181 AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACAGGTGAAGGAGGAGTGAAGTTCAGAACTTTGACACCCCTCTACGCCATCTG 958
Db 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220
QY 959 GATGAGAAGACAGCGAGTGTGACGGGATCACCGAGGAGGAGGAGGAGCTGGGC 1018
Db 221 AspGluLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLeuGly 240
QY 1019 TTCATCGAGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGG 1078
Db 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATCCAGTCCCTGTGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCCAA 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuSerSerAlaLys 280
QY 1139 CAGCTCATCAAGGACATGTAGAGCTCCAGGGTGCAGGTGGGGAAGACAGAGCAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCGTTTGACACATGAGTACTTACTCTGGACTTAGACACATACAGAGCGCTTGAG 1258
Db 301 GlyPheGluAsnMetAspTyrPheThrLeuAspLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACAGGTAAAGATGTGATGTTTACATGTTTACCTTTTGAAGGCGAG 1318
Db 321 AlaIleAspPheGlyThrGlyLysGlyCysAspValThrCysLeuThrPheGluArgGln 340
QY 1319 CGTTCCTCT 1327
Db 341 ArgSerSer 343
```

RESULT 2

US-09-484-970B-171

; Sequence 171, Application US/09484970B

; Patent No. 6426186

; GENERAL INFORMATION:

```
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkumth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 171
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 3575519CD1 (GENE ID 247384)
US-09-484-970B-171
```

```
Alignment Scores:
Pred. No.: 1,69e-149 Length: 353
Score: 1613.00 Matches: 305
Percent Similarity: 97.55% Conservatives: 13
Best Local Similarity: 93.56% Mismatches: 8
Query Match: 56.64% Indels: 0
DB: 4 Gaps: 0
```

US-10-775-649-5 (1-1597) x US-09-484-970B-171 (1-353)

```
QY 299 ATGGATTATAATCTAGCTGATTCCTGATGAAACGCTATTCGAGAACCTGGAGAGCAG 358
Db 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGCTCATCTGCCCTGCCAA 418
Db 21 LeuileCysProileCysLeuGluMetPheThrLysProValValleLeuProCysGln 40
QY 419 CACAACTCTGCCGAAGTGTGCCACGACATCTTCCAGGCTGCGCAATCCCTACTGAGCC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGGGTGGCTCAGTCCATGCTCGAGGTCGTTTCCGTGCGCCCTGCGCCGCT 538
Db 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTCATGATGACCGACCGGCTGTACGGCTGCAGAGGAACCTGCTGTGGGAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAAGCAGAGTGTCCAGTCCGGCCCTGCAGAAAGCCACCCG 658
Db 101 IleleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGACACGACGAGATCAACATCTACTGTCTCAGCTGTGAGGTCGCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTGTGCAAGGTGTTTGGGGCTCACCGGCTGTGAGGTGCGCCCTTGCAA 778
Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAAAGGACAGAGCTGAGTGAAGTAACTGCAATCTCCATGCTGTGGCGGG 838
Db 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAG 898
Db 181 AsnAspArgValGlnThrIleIleThrGlnLeuGluAspSerArgValThrLysGlu 200
QY 899 AATAGCCACAGGTGAAGGAGGAGTGAAGTTCAGAACTTTGACACCCCTCTACCCCATCTG 958
Db 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220
QY 959 GATGAGAAGACAGCGAGTGTGACGGGATCACCGAGGAGGAGGAGGAGCTGGGC 1018
```

```
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnGluLysLysLeuSer 240
QY 1019 TTCATCGAGGCTCTGATCTCTCCAGTACAGGGAGCAGCTGGAAAGTCCACCAAGCTTG 1078
Db 241 PheIleGluAlaLeuIleGlnGlnTyrglnGlnGluGlnLeuAspLysSerThrLysLeuVal 260
QY 1079 GAGACCGGCATCCATCTCCGATGAGCCGAGGGGCTTACCTCTCTCAAGTCCCAAG 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAGACATGTAGAACCTCCAGGGCTGCCAGCTGGGGAAGACAGCA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCGTTTGAAACATGAGCTACTTTACTCTGGACTTAGAACACATAGCAGAGCCCTTGAGG 1258
Db 301 GlyPheGluAsnMetaspPheThrLeuaspLeuGluHisIleAlaAspAlaLeuArg 320
QY 1259 GCCATTGACTTTGGACA 1276
Db 321 AlaIleAspPheGlyThr 326
```

RESULT 3

US-09-908-988B-4

; Sequence 4, Application US/09908988B

; Patent No. 6740751

; GENERAL INFORMATION:

; APPLICANT: OLSON, ERIC

; APPLICANT: SPENCER, JEFFREY A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES

; FILE OF INVENTION: IN STRIATED MUSCLE CELLS

; FILE REFERENCE: MYOG:028US

; CURRENT APPLICATION NUMBER: US/09/908,988B

; CURRENT FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: 60/219,020

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 545

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-908-988B-4

Alignment Scores:

Pred. No.:	2e-100	Length:	545
Score:	1114.50	Matches:	220
Percent Similarity:	66.75%	Conservative:	45
Best Local Similarity:	55.42%	Mismatches:	61
Query Match:	39.13%	Indels:	71
DB:	4	Gaps:	2

US-10-775-649-5 (1-1597) x US-09-908-988B-4 (1-545)

```
QY 80 ATGAGCACTTCTCTGAATTAAGTCTTTCTCCAAAGACAGCAGACCATGATTAATG 139
Db 1 MetSerThrSerLeuAsnTyrlsSerPheSerLysGluGlnGlnThrMetasp----- 18
QY 140 GAAAGCAACTGATCTGTCCCATCTGCCCTAGAGATGTTCCAGAACGCTGTGTCATCTTC 199
Db 18 ----- 18
QY 200 CCTTGCACACAACTGTGCAGGAAATGTGCGGGCCCCCTTGGAGACAAAGACTTG 259
Db 18 ----- 18
QY 260 GTGACGCGAGGTGGCAAGACAGCTCGCATTTCAAAGCAATATGGATTATAAATCTAGCC 319
Db 18 ----- 18
QY 320 ATTCTGTATGGAACGCTATGGAGAACCTGGAGAACGAGCTGATCTGCCCATCTGCGCTG 379
Db 18 ----- 18
```

RESULT 4

US-09-908-988B-2

; Sequence 2, Application US/09908988B

; Patent No. 6740751

; GENERAL INFORMATION:

; APPLICANT: OLSON, ERIC

; APPLICANT: SPENCER, JEFFREY A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES

; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS

; FILE REFERENCE: MYOG:028US

; CURRENT APPLICATION NUMBER: US/09/908,988B

```
Db 19 -----AsnLeuGluLysGlnLeuIleCysProIleCysLeu 30
QY 380 GAGATGTTTACAAAGCCTGTGGTTCATCTGCGCTGCCAACACAACTCTGCGGGAAGTGT 439
Db 31 GluMetPheThrLysProValValIleLeuProCysGlnHisAsnLeuCysArgLysCys 50
QY 440 GCCAACGACATCTTCCAGGCTGCCAATCCCTACTGGACCAACCCGGCGGTGCATGTC 499
Db 51 AlaSerAspIlePheGlnAlaSerAsnProTyrlLeuProThrArgGlyGlyThrThrVal 70
QY 500 ATGCTGTGAGCTGCTTCCGTTGCCCTCGTCGCGCCGATGAAGTGCATCATGACCGGCAC 559
Db 71 AlaSerGlyGlyArgPheArgCysProSerCysArgHisGluValValIleuAspArgHis 90
QY 560 GGGGTGTACGGCCCTCGACAGGAACCTCTGCTGTGGAAAAACATCATTTGACATCTTACAAGCAG 619
Db 91 GlyValTyrglyLeuGlnArgAsnLeuValGluAsnIleIleAspIleTyrlsGln 110
QY 620 GAGTGCTCAGTCGGCCCTCGACAAAGGACCCACCGATGTGCAGGAACACACGAAGAC 679
Db 111 Glu---SerThrArgProGluLysLysLeuAspGlnProMetCysGluGluHisGlu 129
QY 680 GAGAAGATCAACATCTACTGTCTCACGTGTGAGTGCCCTACTTGTCTCTTGTGCAAGTG 739
Db 130 GluArgIleAsnIleTyrlCysLeuAsnCysGluValProThrCysSerLeuCysVal 149
QY 740 TTTGGGGCTCACAGGCCTGTGAGCTTCCCTTTTGCAAAGCATCTTCCAAGGACAGAG 799
Db 150 PheGlyAlaHisLysAspCysGlnValAlaProLeuThrHisValPheGlnArgGlnLys 169
QY 800 ACTGAGCTGAGTAATGTCATCTCCATGCTGTGTGGGGGGAACGACCGAGTGTCAGACGATC 859
Db 170 SerGluLeuSerAspGlyIleAlaValLeuValGlySerAsnAspArgValGlnGlyVal 189
QY 860 ATCTCTCAGCTGGAGGACTCGTCAGAGTGCACCAAGGAGATAGCCACGAGTGAGGAG 919
Db 190 IleSerGlnLeuGluAspThrCysLysThrIleGluGluCysCysArgLysGlnLysGln 209
QY 920 GAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCTCTGGATGAGAGAAGACGAGCTG 979
Db 210 AspLeuCysGluLysPheAspHisLeuTyrglyIleLeuGluGluArgLysThrGluMet 229
QY 980 CTGACGCGGATCAGCAGGAGCAGAGGAGAGAGTGGGCTTCATCGAGGCTCTGATCTTC 1039
Db 230 ThrGlnAlaIleThrArgThrGlnGluLysLeuGluHisValArgThrLeuIleArg 249
QY 1040 CAGTACAGGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTG 1099
Db 250 LysTyrlSerAspHisLeuGluAsnValSerLysLeuValGluSerGlyIleGlnPheMet 269
QY 1100 GATGAGCCCGGAGGGCTTACCTTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATTTGTA 1159
Db 270 AspGluProGluMetAlaValPheIleGluAsnAlaLysThrLeuGlnLysIleVal 289
QY 1160 GAAGCTCTCAAGGGCTGCAGCTGGGGAAGACAGAGCAAGGCTTTGAGAACATGACTTAC 1219
Db 290 GluAlaSerLysAlaPheGlnMetGluLysLeuGluGlnGlyTyrgluIleMetSerAsn 309
QY 1220 TTTACTCTGGACTTAGAACACATAGCAGAGGCTTGGAGGCCATTTGACTTTT 1270
Db 310 PheThrValAsnLeuAsnArgGluLysIleIleArgGluIleAspPhe 326
```

```
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-908-988B-2

Alignment Scores:
Pred. No.: 4,4e-100 Length: 366
Score: 1110.00 Matches: 212
Percent Similarity: 78.53% Conservative: 55
Best Local Similarity: 62.35% Mismatches: 63
Query Match: 38.97% Indels: 10
DB: 4 Gaps: 3

US-10-775-649-5 (1-1597) x US-09-908-988B-2 (1-366)
QY 278 ACAGTCGCATTTCAAGCAATATGGATTATAATCTAGCTGATTCCTGATGGAACGCT 337
Db 4 ThrValGlyPheLys-----ProLeuLeuGlyAspAlaHisAen 16
QY 338 ATGGAGAACTGTGAGAACGAGCTGATCTGCCCATCTGCTGGAGATGTTTACCAGCCT 397
Db 17 MetAspAsnLeuGluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysPro 36
QY 398 GTGGTCATCTGCTGCCAACACACATCTGCGGGAAGTGTGCCAACACATCTTCCAG 457
Db 37 ValValIleLeuProCysGlnHisAenLeuCysArgLysCysAlaAsnAspValPheGln 56
QY 458 GCTGCGAATCCCTACTGACCAACCGGGTGGCTCAGTGTCCATGCTCTGGAGTCTTTC 517
Db 57 AlaSerAsnProLeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPhe 76
QY 518 CGTTGCGCCCTCGTCCGCCATGAAGTGATCATGACCGGCAACGGGTGTACGGCCTCGAG 577
Db 77 ArgCysProSerCysArgHisGluValValLeuAspArgHisGlyValTyrglyLeuGln 96
QY 578 AGAAGCTGTGTGGAACATCATTCATCTACAGCAGAGTGTCTCAGTGGGCC 637
Db 97 ArgAsnLeuLeuValGluAsnIleIleAspIleTyrglyGlnGlu---SerSerArgPro 115
QY 638 CTG-----CAGAAAGCGACCCGATGTGCAGGAACACAGACGAGAGATCAAC 691
Db 116 LeuHisAlaLysAlaGluGlnHisLeuMetCysGluGluHisGluAspGluLysIleAen 135
QY 692 ATCTACTGTCTCACGTGTGAGGTGCTTACTTGTCTTGTGCAAGGTGTTTGGGGCTCAC 751
Db 136 IleTyrglyLeuSerCysGluValProThrCysSerLeuCysLysValPheGlyAlaHis 155
QY 752 CAGGCTGTGAGTGGCTTCCCTTTGAAAGCATCTTCCAAAGACAGAAAGTGTGAGT 811
Db 156 LysAspCysGluValAlaProLeuProThrIleTyrglyArgGlnLysSerGluLeuSer 175
QY 812 AACTGATCTCCATGCTGTGGGGGACCGAGTGCAGACGATCATCTCTCAGCTG 871
Db 176 AspGlyIleAlaMetLeuValAlaGlyAsnAspArgValGlnAlaValIleThrGlnMet 195
QY 872 GAGGACTCTGTGACGATGACCAAGAGAATAGCCACGAGTGAAGGAGGAGTGTGAGT 931
Db 196 GluGluValCysGlnThrIleGluAspAsnSerArgArgGlnLysGlnLeuLeuAenGln 215
QY 932 AGTTTGACACCTCTACCGCATCTCGGATGAGAGAAGAGGAGCTGTGAGCGGATC 991
Db 216 ArgPheGluThrLeuCysAlaValLeuGluGluArgLysGlyGluLeuLeuGlnAlaLeu 235
QY 992 ACGCAGGACGAGGAGAGAGTGGGCTTTCATCGAGGCTCTGATCTCTCAGTACAGGGAG 1051
Db 236 AlaArgGluGlnGluLysLeuGlnArgValArgGlyLeuIleArgGlnTyrglyAsp 255
```

```
QY 1052 CAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCTCCTGGATGAGCCCGGA 1111
Db 256 HisLeuGluGlySerSerLysLeuValGluSerAlaIleGlnSerMetGluGluProGln 275
QY 1112 GGGGCTACCTCTCTCAAGTCCCAAGCAGCTCATCAAGAGCATTTGTAGAGCCTCAAG 1171
Db 276 MetAlaLeuTyrglyLeuGlnGlnAlaLysGluLeuIleAsnLysValGlyAlaMetSerLys 295
QY 1172 GGCTGCCAGCTGGGAAGACAGACAGCAAGGCTTTGAGAACATGACTACTTACTCTGGAC 1231
Db 296 ValGluLeuAlaGlyArgProGluProGlyTyrglySerMetGluGlnPheSerValSer 315
QY 1232 TTAGAACACATAGCAGAGCCTTTGAGGGCCATTTGGGACAGGTAAAGGATGTAT 1291
Db 316 ValGluHisValAlaGluMetLeuArgThrIleAspPheGlnProGlyAlaAlaGlyAsp 335
RESULT 5
US-09-327-983-5
; Sequence 5, Application US/09327983
; Patent No. 6633819
; GENERAL INFORMATION:
; APPLICANT: Rhetsky, Andrey
; TITLE OF INVENTION: GENE DISCOVERY THROUGH COMPARISONS OF
; TITLE OF INVENTION: NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG
; FILE OF INVENTION: GENES AND PROTEINS
; FILE REFERENCE: AP31869 070050.1046
; CURRENT APPLICATION NUMBER: US/09/327,983
; CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-327-983-5

Alignment Scores:
Pred. No.: 1,87e-17 Length: 223
Score: 267.50 Matches: 79
Percent Similarity: 46.69% Conservative: 41
Best Local Similarity: 30.74% Mismatches: 86
Query Match: 9.39% Indels: 51
DB: 4 Gaps: 11

US-10-775-649-5 (1-1597) x US-09-327-983-5 (1-223)
QY 338 ATGGAGAACTGGAGAACGAGCTGATCTGCCCATCTGCTGGAGATGTTTACCAGCCT 397
Db 2 MetGluLeuLeuGluGluAspLeuThrCysProIleCysCysSerLeuPheAspPro 21
QY 398 GTGGTCATCTCCCTGCGCAACACACACCTCTCGCGGAGTGTGCCAACACATCTTCCAG 457
Db 22 ArgVal---LeuProCysSerHisAsnPheCysLysLysLeuGluGlyIleLeuGlu 40
QY 458 GCTGCGAATCCCTACTTGGACCAACCGGCTGCTCAGTGTCTCCATGCTCTGGAGTCTGT 514
Db 41 -----GlySerValArgAsnSerMetTrpArgPro 50
QY 515 -----TTCCGTTGCCCTCTGTCGCCCATGATGATGATCATGACCGGACCGGGGTGTAC 568
Db 51 AlaProPheLysCysProThrCysArgLysGluThr-----SerAlaThrGlyIleAen 68
QY 569 GGCCTGCAGAGAACCTGTGCTGGAAAAACATTCATTGACATCTACAAGCAGGAGTCTCC 628
Db 69 SerLeuGlnValAsnTyrglySerLeuLysGlyIleValGluLysTyrglyAsnLysIle 88
QY 629 AGTCGGCCCTCGCAGAAAGCGACCCACCGATGTGCAAGAAACACGACGAGAGATC 698
Db 89 SerProLysMet-----ProValCysLysGlyHisMetGlyGlnProLeu 103
QY 689 AACATCTACTGTCTACGTGTGAGGTGCTACTTCTCTCTGTCGCAAGTGTGTTGGGCT 748
Db -----
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 15, 2005, 14:48:17 ; Search time 127 Seconds
(without alignments)
9640.710 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 2848

Sequence: 1 ctcgagattacccttacag.....gaaataaattctcgtgcc 1597

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 3420798

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2_1/USPTO spool_p/US10775649/runat_14062005_141113_20778/app_query.fasta_1.1735
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=0 -MODS=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10775649 @CNG 1.1.130 @runat_14062005_141113_20778
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -OSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pcp.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pcp.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pcp.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pcp.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1802	63.3	343	9	US-09-908-988B-6	Sequence 6, Appli
2	1802	63.3	343	16	US-10-775-649-6	Sequence 6, Appli
3	1802	63.3	343	16	US-10-775-627-6	Sequence 21, Appli
4	1671	58.7	351	14	US-10-061-043A-21	Sequence 36, Appli
5	1671	58.7	351	14	US-10-061-043A-36	Sequence 46, Appli
6	1671	58.7	351	14	US-10-061-043A-45	Sequence 46, Appli
7	1671	58.7	351	14	US-10-061-043A-46	Sequence 47, Appli
8	1671	58.7	351	14	US-10-061-043A-47	Sequence 47, Appli
9	1671	58.7	351	15	US-10-060-634C-21	Sequence 21, Appli
10	1671	58.7	351	15	US-10-060-634C-36	Sequence 36, Appli
11	1671	58.7	351	15	US-10-060-634C-45	Sequence 45, Appli
12	1671	58.7	351	15	US-10-060-634C-46	Sequence 46, Appli
13	1671	58.7	351	15	US-10-060-634C-47	Sequence 47, Appli
14	1613	56.6	353	15	US-10-094-749-2861	Sequence 85, Appli
15	1613	56.6	353	15	US-10-221-625-85	Sequence 85, Appli
16	1612.5	56.6	366	9	US-09-764-864-808	Sequence 808, Appli
17	1612	56.6	353	14	US-10-061-043A-48	Sequence 48, Appli
18	1612	56.6	353	15	US-10-060-634C-48	Sequence 48, Appli
19	1583.5	55.6	366	17	US-10-204-921-57	Sequence 57, Appli
20	1562	54.8	340	14	US-10-061-043A-23	Sequence 23, Appli
21	1562	54.8	340	15	US-10-060-634C-23	Sequence 23, Appli
22	1126.5	39.6	452	15	US-10-104-047-2403	Sequence 2403, Ap
23	1126.5	39.6	452	16	US-10-473-574-8	Sequence 8, Appli
24	1126.5	39.6	548	15	US-10-104-047-2643	Sequence 2643, Ap
25	1114.5	39.1	545	9	US-09-908-988B-4	Sequence 4, Appli
26	1114.5	39.1	545	16	US-10-775-649-4	Sequence 4, Appli
27	1114.5	39.1	545	16	US-10-775-627-4	Sequence 2, Appli
28	1110	39.0	366	9	US-09-908-988B-2	Sequence 2, Appli
29	1110	39.0	366	16	US-10-775-649-2	Sequence 2, Appli
30	1110	39.0	366	16	US-10-775-627-2	Sequence 58, Appli
31	1107	38.9	358	10	US-09-890-688-58	Sequence 33, Appli
32	1078	37.9	202	14	US-10-061-043A-33	Sequence 33, Appli
33	1078	37.9	202	15	US-10-060-634C-33	Sequence 37, Appli
34	1074	37.7	396	14	US-10-061-043A-37	Sequence 37, Appli
35	1074	37.7	396	15	US-10-060-634C-37	Sequence 39, Appli
36	1015	35.6	289	14	US-10-061-043A-39	Sequence 39, Appli
37	1015	35.6	289	15	US-10-060-634C-39	Sequence 4, Appli
38	985	34.6	326	15	US-10-250-613-4	Sequence 821, App
39	979.5	34.4	414	9	US-09-764-864-821	Sequence 6102, Ap
40	764	26.8	143	11	US-09-864-408A-6102	Sequence 1280, Ap
41	652.5	22.9	184	9	US-09-764-864-1280	Sequence 1269, Ap
42	504	17.7	122	9	US-09-764-864-1269	Sequence 3552, Ap
43	436.5	15.3	736	15	US-10-108-260A-3552	Sequence 2368, Ap
44	432.5	15.2	552	16	US-10-408-765A-2368	Sequence 4278, Ap
45	432.5	15.2	667	16	US-10-723-860-4278	

ALIGNMENTS

RESULT 1
US-09-908-988B-6
; Sequence 6, Application US/09908988B
; Patent No. US20020127690A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028US
; CURRENT APPLICATION NUMBER: US/09/908, 988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219, 020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-908-988B-6									
Alignment Scores:									
Pred. No.:	2.97e-131	Length:	343						
Score:	1802.00	Matches:	343						
Percent Similarity:	100.00%	Conservative:	0						
Best Local Similarity:	100.00%	Mismatches:	0						
Query Match:	63.27%	Indels:	0						
DB:	9	Gaps:	0						
US-10-775-649-5 (1-1597) x US-09-908-988B-6 (1-343)									
QY	299	ATGGATTATAAATCTAGCCTGATTCTCTGATGGAACCGCTATGAGAACCTTGAGAACGAC	358						
DB	1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20						
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGTATCTGCTGCCCTGCCAA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr	60						
QY	479	AACCGCGTGGCTCAGTGTCCATGTCTGGAGGTCTGTTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCTGTACGGCTGTCAGTCCAGTCCAGTCCAGTCCAGTCCAG	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
QY	599	ATCATTGACATCTACAGCAGGAGTGTCCAGTCCGCGCCCTGCAGAAAGGCACGCCCG	658						
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTGCAAGAACACGACAGACGAGATCAACATCTACTGTCTCAAGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
QY	719	ACTTGCTCTTGTGCACAGTGTGTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCAA	778						
DB	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160						
QY	779	AGCATCTTCCACGACAGACACTGAGTCACTGATCTCCATCTCCATGTGTTGGGGGG	838						
DB	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180						
QY	839	AACGACCGAGTGCACGATCATCTCTCAGCTGAGGACTCTGTCGACAGTGCACCAAGGAG	898						
DB	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200						
QY	899	AATAGCCACCAAGTGAAGGAGGAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCCTG	958						
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
QY	959	GATGAGAAGACGAGCTGCTCTCAGCGATCACGACGAGCAGGAGGAGGAGCTGGGC	1018						
DB	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGlnGln	240						
QY	1019	TTTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG	1078						
DB	241	PheIleGluAlaLeuIleLeuGlnTyrArgGlnGlnLeuGluLysSerThrLysLeuVal	260						
QY	1079	GAGACCGCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCACAAG	1138						
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuSerSerAlaLys	280						
QY	1139	CAGCTCATCAAGACATTGTAGAGCCTCCAGGGCTGCCAGCTGGGGAAGACAGACAA	1198						
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300						
QY	1199	GGCTTTGAGAACATGGACTACTTTTACTCTGAGCTTAGAACACATAGCAGAGGCGTTGAGG	1258						

US-09-908-988B-6									
Alignment Scores:									
Pred. No.:	2.97e-131	Length:	343						
Score:	1802.00	Matches:	343						
Percent Similarity:	100.00%	Conservative:	0						
Best Local Similarity:	100.00%	Mismatches:	0						
Query Match:	63.27%	Indels:	0						
DB:	9	Gaps:	0						
US-10-775-649-5 (1-1597) x US-09-908-988B-6 (1-343)									
QY	299	ATGGATTATAAATCTAGCCTGATTCTCTGATGGAACCGCTATGAGAACCTTGAGAACGAC	358						
DB	1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20						
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGTATCTGCTGCCCTGCCAA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr	60						
QY	479	AACCGCGTGGCTCAGTGTCCATGTCTGGAGGTCTGTTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCTGTACGGCTGTCAGTCCAGTCCAGTCCAGTCCAGTCCAG	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
QY	599	ATCATTGACATCTACAGCAGGAGTGTCCAGTCCGCGCCCTGCAGAAAGGCACGCCCG	658						
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTGCAAGAACACGACAGACGAGATCAACATCTACTGTCTCAAGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
QY	719	ACTTGCTCTTGTGCACAGTGTGTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCAA	778						
DB	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160						
QY	779	AGCATCTTCCACGACAGACACTGAGTCACTGATCTCCATCTCCATGTGTTGGGGGG	838						
DB	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180						
QY	839	AACGACCGAGTGCACGATCATCTCTCAGCTGAGGACTCTGTCGACAGTGCACCAAGGAG	898						
DB	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200						
QY	899	AATAGCCACCAAGTGAAGGAGGAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCCTG	958						
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
QY	959	GATGAGAAGACGAGCTGCTCTCAGCGATCACGACGAGCAGGAGGAGGAGCTGGGC	1018						
DB	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGlnGln	240						
QY	1019	TTTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG	1078						
DB	241	PheIleGluAlaLeuIleLeuGlnTyrArgGlnGlnLeuGluLysSerThrLysLeuVal	260						
QY	1079	GAGACCGCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCACAAG	1138						
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuSerSerAlaLys	280						
QY	1139	CAGCTCATCAAGACATTGTAGAGCCTCCAGGGCTGCCAGCTGGGGAAGACAGACAA	1198						
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300						
QY	1199	GGCTTTGAGAACATGGACTACTTTTACTCTGAGCTTAGAACACATAGCAGAGGCGTTGAGG	1258						

US-09-908-988B-6									
Alignment Scores:									
Pred. No.:	2.97e-131	Length:	343						
Score:	1802.00	Matches:	343						
Percent Similarity:	100.00%	Conservative:	0						
Best Local Similarity:	100.00%	Mismatches:	0						
Query Match:	63.27%	Indels:	0						
DB:	9	Gaps:	0						
US-10-775-649-5 (1-1597) x US-09-908-988B-6 (1-343)									
QY	299	ATGGATTATAAATCTAGCCTGATTCTCTGATGGAACCGCTATGAGAACCTTGAGAACGAC	358						
DB	1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20						
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGTATCTGCTGCCCTGCCAA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr	60						
QY	479	AACCGCGTGGCTCAGTGTCCATGTCTGGAGGTCTGTTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCTGTACGGCTGTCAGTCCAGTCCAGTCCAGTCCAGTCCAG	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
QY	599	ATCATTGACATCTACAGCAGGAGTGTCCAGTCCGCGCCCTGCAGAAAGGCACGCCCG	658						
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTGCAAGAACACGACAGACGAGATCAACATCTACTGTCTCAAGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
QY	719	ACTTGCTCTTGTGCACAGTGTGTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCAA	778						
DB	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160						
QY	779	AGCATCTTCCACGACAGACACTGAGTCACTGATCTCCATCTCCATGTGTTGGGGGG	838						
DB	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180						
QY	839	AACGACCGAGTGCACGATCATCTCTCAGCTGAGGACTCTGTCGACAGTGCACCAAGGAG	898						
DB	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200						
QY	899	AATAGCCACCAAGTGAAGGAGGAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCCTG	958						
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
QY	959	GATGAGAAGACGAGCTGCTCTCAGCGATCACGACGAGCAGGAGGAGGAGCTGGGC	1018						
DB	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGlnGln	240						
QY	1019	TTTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG	1078						
DB	241	PheIleGluAlaLeuIleLeuGlnTyrArgGlnGlnLeuGluLysSerThrLysLeuVal	260						
QY	1079	GAGACCGCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCACAAG	1138						
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuSerSerAlaLys	280						
QY	1139	CAGCTCATCAAGACATTGTAGAGCCTCCAGGGCTGCCAGCTGGGGAAGACAGACAA	1198						
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300						
QY	1199	GGCTTTGAGAACATGGACTACTTTTACTCTGAGCTTAGAACACATAGCAGAGGCGTTGAGG	1258						

US-09-908-988B-6									
Alignment Scores:									
Pred. No.:	2.97e-131	Length:	343						
Score:	1802.00	Matches:	343						
Percent Similarity:	100.00%	Conservative:	0						
Best Local Similarity:	100.00%	Mismatches:	0						
Query Match:	63.27%	Indels:	0						
DB:	9	Gaps:	0						
US-10-775-649-5 (1-1597) x US-09-908-988B-6 (1-343)									
QY	299	ATGGATTATAAATCTAGCCTGATTCTCTGATGGAACCGCTATGAGAACCTTGAGAACGAC	358						
DB	1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20						
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGTATCTGCTGCCCTGCCAA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr	60						
QY	479	AACCGCGTGGCTCAGTGTCCATGTCTGGAGGTCTGTTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCTGTACGGCTGTCAGTCCAGTCCAGTCCAGTCCAGTCCAG	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
QY	599	ATCATTGACATCTACAGCAGGAGTGTCCAGTCCGCGCCCTGCAGAAAGGCACGCCCG	658						
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTGCAAGAACACGACAGACGAGATCAACATCTACTGTCTCAAGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
QY	719	ACTTGCTCTTGTGCACAGTGTGTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCAA	778						
DB	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160						
QY	779	AGCATCTTCCACGACAGACACTGAGTCACTGATCTCCATCTCCATGTGTTGGGGGG	838						
DB	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180						
QY	839	AACGACCGAGTGCACGATCATCTCTCAGCTGAGGACTCTGTCGACAGTGCACCAAGGAG	898						
DB	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200						
QY	899	AATAGCCACCAAGTGAAGGAGGAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCCTG	958						
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
QY	959	GATGAGAAGACGAGCTGCTCTCAGCGATCACGACGAGCAGGAGGAGGAGCTGGGC	1018						
DB	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGlnGln	240						
QY	1019	TTTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG	1078						
DB	241	PheIleGluAlaLeuIleLeuGlnTyrArgGlnGlnLeuGluLysSerThrLysLeuVal	260						
QY	1079	GAGACCGCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCACAAG	1138						
DB	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuSerSerAlaLys	280						
QY	1139	CAGCTCATCAAGACATTGTAGAGCCTCCAGGGCTGCCAGCTGGGGAAGACAGACAA	1198						
DB	281	GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300						
QY	1199	GGCTTTGAGAACATGGACTACTTTTACTCTGAGCTTAGAACACATAGCAGAGGCGTTGAGG	1258						

US-09-908-988B-6									
Alignment Scores:									
Pred. No.:	2.97e-131	Length:	343						
Score:	1802.00	Matches:	343						
Percent Similarity:	100.00%	Conservative:	0						
Best Local Similarity:	100.00%	Mismatches:	0						
Query Match:	63.27%	Indels:	0						
DB:	9	Gaps:	0						
US-10-775-649-5 (1-1597) x US-09-908-988B-6 (1-343)									
QY	299	ATGGATTATAAATCTAGCCTGATTCTCTGATGGAACCGCTATGAGAACCTTGAGAACGAC	358						
DB	1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20						
QY	359	CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGTATCTGCTGCCCTGCCAA	418						
DB	21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40						
QY	419	CACAACTCTGCCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478						
DB	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr	60						
QY	479	AACCGCGTGGCTCAGTGTCCATGTCTGGAGGTCTGTTTCCGTTGCCCTCGTCCGCCAT	538						
DB	61	AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis	80						
QY	539	GAAGTGATCATCGACCGGCTGTACGGCTGTCAGTCCAGTCCAGTCCAGTCCAGTCCAG	598						
DB	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100						
QY	599	ATCATTGACATCTACAGCAGGAGTGTCCAGTCCGCGCCCTGCAGAAAGGCACGCCCG	658						
DB	101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120						
QY	659	ATGTGCAAGAACACGACAGACGAGATCAACATCTACTGTCTCAAGTGTGAGTGCCT	718						
DB	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140						
QY	719	ACTTGCTCTTGTGCACAGTGTGTTGGGCTCACAGGCTGTGAGTGTGCCCTTTGCAA	778						
DB	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160						
QY	779	AGCATCTTCCACGACAGACACTGAGTCACTGATCTCCATCTCCATGTGTTGGGGGG	838						
DB	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180						
QY	839	AACGACCGAGTGCACGATCATCTCTCAGCTGAGGACTCTGTCGACAGTGCACCAAGGAG	898						
DB	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200						
QY	899	AATAGCCACCAAGTGAAGGAGGAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCCTG	958						
DB	201	AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu	220						
QY	959	GATGAGAAGACGAGCTGCTCTCAGCGATCACGACGAGCAGGAGGAGGAGCTGGGC	1018						
DB	221	AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnGlnGlnGln	240						
QY	1019	TTTCATCGAGGCTCTGATCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG	1078						
DB	241	PheIleGluAlaLeuIleLeuGlnTyrArgGlnGlnLeuGluLysSerThrLysLeuVal	260						
QY	1079	GAGACCGCATCCAGTCCCTGGATGAGCCCGGAGGGGCTACCT							

301	GlyPheGluAsnMetAspTyrPheThrLeuAspLeuGluHisIleAlaGluAlaLeuArg	320
1259	GCCATTGACTTTGGACAGGTAAAGATGTGATGTTTACATGTTTGACCTTTGAAAGGCAG	1318
321	AlaIleAspPheGlyThrGlyLysGlyCysAspValThrCysLeuThrPheGluArgGln	340
1319	CGTTCTCT 1327	
341	ArgSerSer 343	
RESULT 2		
US-10-775-649-6		
; Sequence 6, Application US/10775649		
; Publication No. US20040132160A1		
; GENERAL INFORMATION:		
; APPLICANT: OLSON, ERIC		
; APPLICANT: SPENCER, JEFFREY A.		
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES		
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS		
; FILE REFERENCE: MYOG-028USD2		
; CURRENT APPLICATION NUMBER: US/10/775,649		
; CURRENT FILING DATE: 2004-02-10		
; PRIOR APPLICATION NUMBER: 09/908,988		
; PRIOR FILING DATE: 2001-07-18		
; PRIOR APPLICATION NUMBER: 60/219,020		
; PRIOR FILING DATE: 2000-07-18		
; NUMBER OF SEQ ID NOS: 6		
; SOFTWARE: PatentIn ver. 2.1		
; SEQ ID NO 6		
; LENGTH: 343		
; TYPE: PRT		
; ORGANISM: Mus musculus		
US-10-775-649-6		
Alignment Scores:		
SeqPred. No.: 2,97e-131 Length: 343		
Score: 1802.00 Matches: 343		
Percent Similarity: 100.00% Conservative: 0		
Best Local Similarity: 100.00% Mismatches: 0		
Query Match: 63.27% Indels: 0		
DB: 16 Gaps: 0		
US-10-775-649-5 (1-1597) x US-10-775-649-6 (1-343)		
299	ATGATTATAAATCTAGCTGATTCTCTGATGGAACCGCTATGAGAACCTTGAGAAAGCAG	358
1	MetAspTyrLysSerSerLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln	20
359	CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCTGTGGTGTATCTGCTCCCTGCCAA	418
21	LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln	40
419	CACAACTCTGCCGGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478
41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr	60
479	AACCGCGTGGCTCAGTGTCCATGTCTGGAGGTCTGCGTTCGGTTCGCCCTCGTCCGCCAT	538
61	AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis	80
539	GAAGTGATCATCGACCGGCTGTACGGCTGTCAGGAACTCTGCTGGTGGTGGTGGTGGTGG	598
81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100
599	ATCATTGACATCTACAGCAGGAGTGTCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG	658
101	IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120
659	ATGTCGAGGAAACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG	718
121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140

QY 719 ACTTGCTCTTGTGCAAGTGTGTTGGGCTCACCAGGCTGTGAGGTGGCCCTTTGCAA 778
Db 141 ThrCysSerLeuCyLeysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACAGAGACTGAGCTGAGTAACTCATCTCCATCTGCTGGCGGG 838
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAenCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACATCATCTCTCAGCTGGAGGACTCGTGAGAGTACACCAAGGAG 898
Db 181 AenAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGTGAAGAGAGCTGAGTCAAGATTGACACCTCTACGCCATCTCTG 958
Db 201 AenSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyAlaIleLeu 220
QY 959 GATGAGAAGAGAGCGAGCTGTGACGGGATCACGACGAGGACGAGAGAGCTGGGC 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuGly 240
QY 1019 TTCATCGAGGCTCTGATCCTCCAGTACAGGGACGAGCTGGAAAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuIleLeuGlnTyArgGluGlnLeuGluLysSerThrLysVal 260
QY 1079 GAGACCGCATCCAGTCCCTGATGAGCCGAGCGGGGCTACCTCTCTCAAGTCCCAAG 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLeuSerSerAlaLys 280
QY 1139 CAGCTCATCAGAGCATTTAGAACCTCCAGGCTGCCAGCTGGGGAAGACAGACAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyThrGluGln 300
QY 1199 GCGTTTGAAACATGGACTACTTTACTCTGGACTTTAGAACACATACGAGGCGCTTGAGG 1258
Db 301 GlyPheGluAenMetAspTyPheThrLeuAspLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGATTTGGACAGGTTAAAGATGTGATTTACATGTTGACCTTTGAAAGGCGAG 1318
Db 321 AlaIleAspPheGlyThrGlyLysGlyCysAspValThrCysLeuThrPheGluArgGln 340
QY 1319 CQTTCCTCT 1327
Db 341 ArgSerSer 343

RESULT 3

US-10-775-627-6
; Sequence 6 Application US/10775627
; Publication No. US20040142446A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG:028USD1
; CURRENT APPLICATION NUMBER: US/10/775,627
; CURRENT FILING DATE: 2004-02-10
; PRIOR FILING DATE: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-775-627-6
Alignment Scores:
Pred. No.: 2,97e-131 Length: 343
Score: 1802.00 Matches: 343
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 63.27% Indels: 0
DB: 16 Gaps: 0
US-10-775-649-5 (1-1597) x US-10-775-627-6 (1-343)
QY 299 ATGGATTTAATCTAGCCTGATTCCTGATGGAACGCTATGGAGAACTCTGGAGAGCAG 358
Db 1 MetAspTyLysSerSerLeuIleProAspGlyAenAlaMetGluAenLeuGluLysGln 20
QY 359 CTGATCTCCCCCATCTGCTGGAGATGTTTACCAAGCCTGTGGTTCATCTGCGCCCTGCCAA 418
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACCTCTCCGGAAGTGTCCAAACGACATCTTCCAGGCTGCCAATCCCTTACTGGACC 478
Db 41 HisAenLeuCysArgLysCysAlaAenAspIlePheGlnAlaAaAenProTyTrpThr 60
QY 479 AACCGCGTGGCTCAGTCTCCATCTCTGAGAGTGTGTTCCGTTGCTCCCTCGTCGCCCAT 538
Db 61 AenArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGGACCGGCACGGGTGTACGGCTTCAGAGAGAACTCTGTTGGTGAAGAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyArgLysGlnArgAenLeuValGluAen 100
QY 599 ATCATTTGATCTTACAAGCAGGAGTGTCCAGTCGCGCCCTGCAGAAAGGACGACCCG 658
Db 101 IleIleAspIleTyLysLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAGGAACACGAGACGAGAGATCAACATCTACTGTCTCAGCTGTGAGTGCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAenIleTyCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTTGTGCAAGTGTGTTGGGCTCACCAGGCTGTGAGGTTGCCCTTTGCAA 778
Db 141 ThrCysSerLeuCyLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACAGAGACTGAGTGAAGTAACTCATCTCCATGCTGCTGGCGGG 838
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAenCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACATCATCTCTCAGCTGGAGGACTCGTGAGAGTACACCAAGGAG 898
Db 181 AenAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGAGTGAAGAGGAGCTGAGTCAAGATTGACACCTCTTACGCCATCTCTG 958
Db 201 AenSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyAlaIleLeu 220
QY 959 GATGAGAAGAGAGCGAGCTCTGCGCGGATCACGACGAGGACGAGAGAGCTGGGC 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuGly 240
QY 1019 TTCATCGAGGCTCTGATCCTCCAGTACAGGGACGAGCTGGAAAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuIleLeuGlnTyArgGluGlnLeuGluLysSerThrLysVal 260
QY 1079 GAGACCGCATCCAGTCTCTCGATGAGCCGCGGGGCTTACCTCTCTCAAGTGCACAG 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyAlaThrPheLeuSerSerAlaLys 280
QY 1139 CAGCTCATCAGAGCATTTAGAACCTCCAGGCTGCCAGCTGGGGAAGACAGACAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyThrGluGln 300
QY 1199 GCGTTTGAAACATGGACTACTTTACTCTGGACTTTAGAACACATACGAGGCGCTTGAGG 1258
Db 301 GlyPheGluAenMetAspTyPheThrLeuAspLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGATTTGGACAGGTTAAAGATGTGATTTACATGTTGACCTTTGAAAGGCGAG 1318
Db 321 AlaIleAspPheGlyThrGlyLysGlyCysAspValThrCysLeuThrPheGluArgGln 340
QY 1319 CQTTCCTCT 1327
Db 341 ArgSerSer 343


```
QY 359 CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGGTCACTCTGCTGCCCA 418
Db |||||
QY 21 LeuileCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
Db |||||
QY 419 CACACCTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTACTGACC 478
Db |||||
QY 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
Db |||||
QY 479 AACCCGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCTGCTGCCCAT 538
Db |||||
QY 61 AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80
Db |||||
QY 539 GAAGTGATCATGACCGGACCGGTGTACGCGCTGCAGAGAACCTGCTGGTGAAGAAC 598
Db |||||
QY 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
Db |||||
QY 599 ATCATTGTACATCAACGAGAGTCTCCAGTCCGCGCCCTGCAGAAAGCGACCCG 658
Db |||||
QY 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
Db |||||
QY 659 ATGTGCAAGGAACACGAGACGAGAGATCAACATCTACTGTCTCACGTGTGAGTGCCT 718
Db |||||
QY 121 MetCysLysGluHisGluAspGlyValTyrGlyLeuGlnArgAsnLeuValPro 140
Db |||||
QY 719 ACTTCTCTCTGTGCAAGTGTGTTGGGCTCACAGGCTGTGAGGTTGCCCTTTGCAA 778
Db |||||
QY 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
Db |||||
QY 779 AGCATCTTCCAGGACAGAGACTGAGTGAAGTGTGAGTGAAGTGTGAGTGAAGTGTG 838
Db |||||
QY 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
Db |||||
QY 839 AACGACCGAGTGCAGACGATCTCTCAGCTGGAGGACTCTGTGACAGAGTACCAAGGAG 898
Db |||||
QY 181 AsnAspArgValGlnThrIleLeuSerGlnLeuGluAspSerCysArgValThrLysGlu 200
Db |||||
QY 899 AATAGCCACCGAGTGAAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 958
Db |||||
QY 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
Db |||||
QY 959 GATGAGAGAGAGAGAGAGTCTGCTGAGCGGATCAAGCAGGAGCAGGAGAGAGTGGGC 1018
Db |||||
QY 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGluGlnGluLysLeuAsp 240
Db |||||
QY 1019 TTCATCTGAGGCTCTGATCTCTCCAGTACAGGAGAGCTGGAAGTGCACCAAGCTTGTG 1078
Db |||||
QY 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
Db |||||
QY 1079 GAGACCGCCCATCCAGTCTCTGATGAGCGCGGAGGCTTACCTCTCTCAAGTCCCAAG 1138
Db |||||
QY 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
Db |||||
QY 1139 CAGCTCATCAAGAGATGTAGAAGCTTCAAGGCTGCCAGCTGCCAGGAGAGAGAGAG 1198
Db |||||
QY 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
Db |||||
QY 1199 GCCTTTGAGACATGAGTACTTCTTCTGGAAGTGTAGAACACATAGCAGAGGCTTGGAG 1258
Db |||||
QY 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
Db |||||
QY 1259 GCCATTGACTTTGGGACA 1276
Db |||||
QY 321 AlaIleAspPheGlyThr 326
Db |||||
RESULT 6
US-10-061-043A-45
; Sequence 45, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
```

```
; CURRENT APPLICATION NUMBER: US/10/061.043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 351
; TYPE: PRT
; ORGANISM: rat
US-10-061-043A-45

Alignment Scores:
Pred. No.: 4,6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 14 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-061-043A-45 (1-351)
QY 299 ATGGATTATAATCTAGCTCTGATTCCTGATGAAACGCTATGGAGAACCTGGAGAGCAG 358
Db |||||
QY 1 MetAspTyrLysSerGlyLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20
Db |||||
QY 359 CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGGTCACTCTGCTGCCCA 418
Db |||||
QY 21 LeuileCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
Db |||||
QY 419 CACACCTCTGCCGAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTACTGAGCC 478
Db |||||
QY 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
Db |||||
QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGGAGTCTGTTCCGTTGCCCTCTGCTGCCCAT 538
Db |||||
QY 61 AsnArgGlyGlySerValSerMetSerGlyArgPheArgCysProSerCysArgHis 80
Db |||||
QY 539 GAAGTGATCATGACCGGACCGGTGTACGCGCTGCAGAGAACCTGCTGGTGAAGAAC 598
Db |||||
QY 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
Db |||||
QY 599 ATCATTGTACATCAACGAGAGTGTCCAGTCCGCGCCCTGCAGAAAGCGACCCG 658
Db |||||
QY 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
Db |||||
QY 659 ATGTCAGAGAACACGAGAGACTGAGTGAAGTGTGAGTGAAGTGTGAGTGAAGTGTG 718
Db |||||
QY 121 MetCysLysGluHisGluAspGlyValTyrGlyLeuGlnArgAsnLeuValPro 140
Db |||||
QY 719 ACTTCTCTCTGTGCAAGTGTGTTGGGCTCACAGGCTGTGAGGTTGCCCTTTGCAA 778
Db |||||
QY 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
Db |||||
QY 779 AGCATCTTCCAGGACAGAGACTGAGTGAAGTGTGAGTGAAGTGTGAGTGAAGTGTG 838
Db |||||
QY 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
Db |||||
QY 839 AACGACCGAGTGCAGACGATCTCTCAGCTGGAGGACTCTGTGACAGAGTACCAAGGAG 898
Db |||||
QY 181 AsnAspArgValGlnThrIleLeuSerGlnLeuGluAspSerCysArgValThrLysGlu 200
Db |||||
QY 899 AATAGCCACCGAGTGAAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 958
Db |||||
QY 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
Db |||||
QY 959 GATGAGAGAGAGAGAGTCTGCTGAGCGGATCAAGCAGGAGCAGGAGAGAGTGGGC 1018
Db |||||
QY 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGluGlnGluLysLeuAsp 240
Db |||||
QY 1019 TTCATCTGAGGCTCTGATCTCTCCAGTACAGGAGAGCTGGAAGTGCACCAAGCTTGTG 1078
Db |||||
QY 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
Db |||||
QY 1079 GAGACCGCCCATCCAGTCTCTGATGAGCGCGGAGGCTTACCTCTCTCAAGTCCCAAG 1138
Db |||||
QY 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
Db |||||
QY 1139 CAGCTCATCAAGAGATGTAGAAGCTTCAAGGCTGCCAGCTGCCAGGAGAGAGAGAG 1198
Db |||||
QY 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
Db |||||
QY 1199 GCCTTTGAGACATGAGTACTTCTTCTGGAAGTGTAGAACACATAGCAGAGGCTTGGAG 1258
Db |||||
QY 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
Db |||||
QY 1259 GCCATTGACTTTGGGACA 1276
Db |||||
QY 321 AlaIleAspPheGlyThr 326
Db |||||
```

QY 1019 TTTCATCGAGGCTCTGATCTCCTCAGTACAGGAGCAGCTGAAAGTCCACCAAGCTTGTG 1078
Db 241 PheileGluAlaLeulleuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATTCAGTCCCTGGATAGCCGAGGGCTACCTCTCTCAAGTGCACAG 1138
Db 261 GluThrAlaileGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAAGAGCATCTAGNAGCTCCNAGGGCTGCAGCTGGGAGACAGACAA 1198
Db 281 ProLeulleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GGCTTTGAGAACATGACTACTTTACTCTGGACTTAGAACACATAGCAGAGCGCTTGAGG 1258
Db 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaileAspPheGlyThr 326
RESULT 7
US-10-061-043A-46
; Sequence 46, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; TYPE: PRT
; ORGANISM: rat
US-10-061-043A-46
Alignment Scores:
Pred. No.: 4.6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 14 Gaps: 0
US-10-775-649-5 (1-1597) x US-10-061-043A-46 (1-351)
QY 299 ATGGATTATAAATCTGATCTGATCGAAGCTGATGAAACGCTATGAGAACCTTGAGAGACAG 358
Db 1 MetAspTyrLysSerGlyLeulleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCCTGTGTCTCTGCTGCCCTGCCAA 418
Db 21 LeulleCysProilleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACNACCTCTGCCGAGGTGCGCAACGACATCTTCAGGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCCGGGTGGCTCAGTGTCCATGTCTGGAGGTGTTCCGTTCGCCCTCGTCCGCCCAT 538
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGACCGGCACCGGGGTGTACGGCTTCAGAGGAACCTGTGTGGAAAC 598

Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAGCAGGAGTGCTCCAGTCCGCCCTGCAGAAAGGCAGCCACCCG 658
Db 101 IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGCAACACAGAACGAGAGATCAACATCTACTGTCTCAGCTGTGAGGTGCCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCCTTGTCAAGGTGTTTGGGCTCACCGGCTGTGAGGTTCCTCCCTTTGCCAA 778
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAGGACAGAGACTGAGCTGAGTAACTGATCTCCATGCTGGTGGGGGG 838
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCATCTCAGCTGGAGGACTCGTGACAGGTGACCAAGGAG 898
Db 181 AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGGTGAAGGAGGAGTGAAGTCAAGTTTGAACACCTCTACGCCATCTCTG 958
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
QY 959 GATGAGAAAGAGCGAGCTGCTGCAGCGGATCCAGCAGGACGAGCAGGAGGAGCTGGGC 1018
Db 221 AspGluLysLysSerGlnLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuAsp 240
QY 1019 TTTCATCGAGGCTCTGATCTCCTCAGTACAGGAGCAGCTGAAAAGTCCACCAAGCTTGTG 1078
Db 241 PheileGluAlaLeulleuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATTCAGTCCCTGATGAGCCGAGGGCTACCTTCTCTCAAGTGCACAG 1138
Db 261 GluThrAlaileGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAAGAGCATCTGAGACGCTCCAGGCTCCAGGCTGCGAGGAGGAGACAGACAA 1198
Db 281 ProLeulleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GGCTTTGAGAACATGACTACTTTACTCTGGACTTAGAACACATAGCAGAGCGCTTGAGG 1258
Db 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaileAspPheGlyThr 326
RESULT 8
US-10-061-043A-47
; Sequence 47, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 351
; TYPE: PRT

; ORGANISM: rat			
US-10-061-043A-47			
Alignment Scores:			
Pred. No.:	4-6e-121	Length:	351
Score:	1671.00	Matches:	319
Percent Similarity:	98.16%	Conservative:	1
Best Local Similarity:	97.85%	Mismatches:	6
Query Match:	58.67%	Indels:	0
DB:	14	Gaps:	0
US-10-775-649-5 (1-1597) x US-10-061-043A-47 (1-351)			
QY	299	ATGGATTATAATCTAGCTGATCTCTGATGAACCGCTATCGAGAACCTGAGAACGAC	358
Db	1	MetAspTyrLysSerGlyLeuileProAspGlyAsnAlaMetGluAsnLeuGluysGln	20
QY	359	CTGATCTGCCCATCTGCTGAGATGTTTACCAAGCCTGTGTCATCTGCGCCCTGCCAA	418
Db	21	LeuileCysProileCysLeuGluMetPheThrLysProValValleLeuProCysGln	40
QY	419	CACAACTCTGCGGAAGTGTCCACGACATCTCCAGGCTGCGAATCCCTACTGGACC	478
Db	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr	60
QY	479	AACCGCGTGGCTCAGTGTCCATGTCTGAGAGTCGTTTCCGTGCGCCCTCGTCCGCCAT	538
Db	61	AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis	80
QY	539	GAAGTGATCATGGACCGGACCGGGGTATCGCCCTGCAGAGAACCTGCTGTGGAAAC	598
Db	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100
QY	599	ATCATTGATCATCTACAAGCAGGAGTGTCCAGTCCGCCCCCTCAGAAAGCGCAGCCCG	658
Db	101	IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120
QY	659	ATGTCAAGGAACACGAAGACGAGAAGATCAACTACTGTCTCACTGTGTGAGGTGCCT	718
Db	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140
QY	719	ACTTGCTCTCTGTGCAAGGTGTTGGGCTCACAGGCTGTGAGGTGCCCTTTGCCAA	778
Db	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160
QY	779	AGCATCTTCCAAAGGACAGAAGACTGAGCTGAGTAAGTCACTGCTCACTGCTGAGGTGCCT	838
Db	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180
QY	839	AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGCAAGAGTGACCAAGGAG	898
Db	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200
QY	899	AATAGCCACAGGTGAAGAGGAGCTGAGTCAAGTTTGACACCTCTACGCCATCTGTG	958
Db	201	AsnSerHisGlnValLysGluGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu	220
QY	959	GATGAGAACAAGCGAGCTGTGCAAGCGATCACGACGAGCAGGAGGAGAGCTGGGC	1018
Db	221	AspGluLysLysSerGlnLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnLysLeuAsp	240
QY	1019	TTTCATCGAGGCTCTGATCTCTCCAGTACAGGAGCAGCTCGGAAAGTCCACCAAGCTTGTG	1078
Db	241	PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal	260
QY	1079	GAGACCGCATTCAGTCCCTGAGTGAAGCCCGAGGGGGCTACCTTCTCTCAAGTGCACAG	1138
Db	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys	280
QY	1139	CAGCTCATCAAGCAATCTGAGAGCCTCCAGGGCTGCAGCTGGGGAAGACAGACAA	1198
Db	281	ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300

; ORGANISM: rat			
US-10-061-043A-47			
Alignment Scores:			
Pred. No.:	4-6e-121	Length:	351
Score:	1671.00	Matches:	319
Percent Similarity:	98.16%	Conservative:	1
Best Local Similarity:	97.85%	Mismatches:	6
Query Match:	58.67%	Indels:	0
DB:	14	Gaps:	0
US-10-775-649-5 (1-1597) x US-10-060-634C-21 (1-351)			
QY	299	ATGGATTATAATCTAGCTGATCTCTGATGAACCGCTATCGAGAACCTGAGAACGAC	358
Db	1	MetAspTyrLysSerGlyLeuileProAspGlyAsnAlaMetGluAsnLeuGluysGln	20
QY	359	CTGATCTGCCCATCTGCTGAGATGTTTACCAAGCCTGTGTCATCTGCGCCCTGCCAA	418
Db	21	LeuileCysProileCysLeuGluMetPheThrLysProValValleLeuProCysGln	40
QY	419	CACAACTCTGCGGAAGTGTCCAAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC	478
Db	41	HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr	60
QY	479	AACCGCGTGGCTCAGTGTCCATGTCTGAGAGTCGTTTCCGTGCGCCCTCGTCCGCCAT	538
Db	61	AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis	80
QY	539	GAAGTGATCATGGACCGGACCGGGGTATCGCCCTGCAGAGAACCTGCTGTGGAAAC	598
Db	81	GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn	100
QY	599	ATCATTGATCATCTACAAGCAGGAGTGTCCAGTCCGCCCCCTCAGAAAGCGCAGCCCG	658
Db	101	IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro	120
QY	659	ATGTCAAGGAACACGAAGACGAGAAGATCAACATCTACTGTCTCACTGCTGAGGTGCCT	718
Db	121	MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro	140
QY	719	ACTTGCTCTCTGTGCAAGGTGTTGGGCTCACAGGCTGTGAGGTGCCCTTTGCCAA	778
Db	141	ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln	160
QY	779	AGCATCTTCCAAAGGACAGAAGACTGAGCTGAGTAAGTCACTGCTCACTGCTGAGGTGCCT	838
Db	161	SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly	180
QY	839	AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGCAAGAGTGACCAAGGAG	898
Db	181	AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu	200
QY	899	AATAGCCACAGGTGAAGAGGAGCTGAGTCAAGTTTGACACCTCTACGCCATCTGTG	958
Db	201	AsnSerHisGlnValLysGluGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu	220
QY	959	GATGAGAACAAGCGAGCTGTGCAAGCGATCACGACGAGCAGGAGGAGAGCTGGGC	1018
Db	221	AspGluLysLysSerGlnLeuLeuGlnArgIleThrGlnGlnGlnGlnGlnLysLeuAsp	240
QY	1019	TTTCATCGAGGCTCTGATCTCTCCAGTACAGGAGCAGCTCGGAAAGTCCACCAAGCTTGTG	1078
Db	241	PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal	260
QY	1079	GAGACCGCATTCAGTCCCTGAGTGAAGCCCGAGGGGGCTACCTTCTCTCAAGTGCACAG	1138
Db	261	GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys	280
QY	1139	CAGCTCATCAAGCAATCTGAGAGCCTCCAGGGCTGCAGCTGGGGAAGACAGACAA	1198
Db	281	ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln	300

Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAAGGACAGAGACTGAGTAACTGTCATCTCCATCTGCTGGCGGG 838
Db 161 SerilePheGlnGlyGlnThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGACAGCATCTCTCAGCTGGAGACTCGTGCAGAGTGACCAAGAG 898
Db 181 AsnAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 ATAGCCACAGGTGAAGGAGGAGTGAGTCAGAAGTTTGACACCTCTACGCCATCTCG 958
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyralaileLeu 220
QY 959 GATGAAAGAACCGAGCTGCTGCAGCGGATCCACGAGGAGCAGGAGGAGCTGGGC 1018
Db 221 AspGluLysSerGlnLeuGluGlnArgIleThrGlnGlnGluGlnLysLeuAsp 240
QY 1019 TTCATCGAGGCTGTGATCTCTCCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG 1078
Db 241 PheileGluAlaLeuileLeuGlnTyArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATCCAGTCCCTGATGAGCCCGAGGGGCTACCTTCTCTCAAGTGCAG 1138
Db 261 GluThrAlaileGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAAGAGCATTGAGAGCTCCAGGGCTCCAGGGCTGCGAGGAGCAGACAA 1198
Db 281 ProLeuileLysSerileValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GGCTTTGAGAACATGGACTACTTACTCTGGACTTAGAACACATAGCAGGCGCTTGAGG 1258
Db 301 GlyPheGluAsnMetAspTyPheThrLeuAsnLeuGluHisileAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaileAspPheGlyThr 326

Alignment Scores:
Pred. No.: 4,6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 15 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-060-634C-36 (1-351)

QY 299 ATGGATTATAAATCTAGCCTGATTCCTGATGAAACGCTATGAGAACCTGGAGAGCAG 358
Db 1 MetAspTyLysSerGlyLeuileProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTGCTGAGATGTTTACAGCCTGTGTGTCATCTGCTGCCCTGCCAA 418
Db 21 LeuileCysProileCysLeuGluMetPheThrLysProValIleLeuProCysGln 40
QY 419 CACACCTCTGCGGGAAGTGCACACGACATCTCCAGGCTCGCAATCCCTACTCTGGACC 478
Db 41 HisAsnLeuLysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyTrpThr 60
QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGAGAGTCTGTTCCGTTCGCCCTCGTCCGCCAT 538
Db 61 AsnArgGlyLysSerValSerMetSerGlyLysArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTATCATGGACCGGACCGGGGTACGGCTGCAGAGAACCTGCTGTGTGGAAAC 598
Db 81 GluValileMetAspArgHisGlyValTyGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTTGACATCTACAAGCAGGAGTCTCCAGTCCGCCCTGCAGAAAGCGACCCCG 658
Db 101 IleileAspIleTyLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGAACACAGACAGAGAGATCAACATCTACTGTCTCACGTGTGAGGTGCCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyLysLeuThrCysGluValPro 140
QY 719 ACTGCTCTCTGTGCAAGGTGTTGGGCTCACAGGCCCTGTGAGGTGCCCTTTGGCAA 778
Db 141 ThrCysSerLeuLysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 ASCATCTTCCAAAGGACAGAGACTGAGCTGAGTAACTGTCATCTCCATGCTGTGGCGGG 838
Db 161 SerilePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCACAGCATCTCTCAGCTGGAGACTCGTGCAGAGTGACCAAGGAG 898
Db 181 AsnAspArgValGlnThrIleileSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 ATAGCCACCGGTGAAGGAGGAGCTGAGTACAGAGTTTGACACCTCTACGCCATCTCTG 958
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyralaileLeu 220
QY 959 GATGAAAGAACGAGCAGCTGCTGCAGCGGATCCACGAGGAGCAGGAGGAGCTGGGC 1018
Db 221 AspGluLysSerGlnLeuGluGlnArgIleThrGlnGlnGlnGluGlnLysLeuAsp 240
QY 1019 TTCATCGAGGCTCTGATCTCTCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTGTG 1078
Db 241 PheileGluAlaLeuileLeuGlnTyArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATCCAGTCCCTGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCAG 1138
Db 261 GluThrAlaileGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAAGAGCATTGAGAGCTCCAGGGCTGCGAGCTGGGGAAGCAGAGCAA 1198
Db 281 ProLeuileLysSerileValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GGCTTTGAGAACATGGACTACTTACTCTGGACTTAGAACACATAGCAGGCGCTTGAGG 1258
Db 301 GlyPheGluAsnMetAspTyPheThrLeuAsnLeuGluHisileAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaileAspPheGlyThr 326

RESULT 11
US-10-060-634C-45
; Sequence 45, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:

```
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 45
; LENGTH: 351
; TYPE: PRT
; ORGANISM: rat
US-10-060-634C-45
Alignment Scores:
Pred. No.: 4.6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservatives: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 15 Gaps: 0
US-10-775-649-5 (1-1597) x US-10-060-634C-45 (1-351)
QY 299 ATGGATTATAATCTAGCTGATTCCTGATGAACGCTATGAGAACCTGAGAACGAG 358
Db 1 MetAspTyrLysSerGlyLeuLeuProAspGlyAsnAlaMetGluAsnLeuGluysGln 20
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGCTCATCTGCTGCCCAA 418
Db 21 LeuileCysProileCysLeuGluMetPheThrLysProValIleLeuProCysGln 40
QY 419 CACAACCTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGGGTGGCTGAGTGCATGTCGTGAGTGCTGTTCCGTTGCTGCTGCTGCGCCCAT 538
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGACCGCGGCGGTACGCGCTGCAGAGAACCTGCTGTGGAAAC 598
Db 81 GluValIleMeCaspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGGAGTGCTCCAGTCGGCCCTCGCAGAAAGCAGCCCGG 658
Db 101 IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGAACAGCAAGACAGAGATCAATCTACTGCTCACTGCTCAGGTGAGTGCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTGCAAGTGTTGGGCTCACCGGCTCACCGGCTGTGAGTTGCCCTTTGCA 778
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTCTTCAAGGACAGAAAGACTGAGCTGAGTAACCTGATCTCCATGCTGCTGGGGG 838
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGACAGCATCATCTCTCAGCTGGAGGACTCTGTGAGAGTACCAGGAG 898
Db 181 AsnAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGTGAAGGAGGCTGAGTACAGAGTTTGACACCTCTTACGCCATCTG 958
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
```

```
959 GATGAGAAAGAGAGCGAGCTGCTGACGCGGATCACGCGAGGACGAGGAGAGCTGGGC 1018
221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuAsp 240
1019 TTCATCGAGGCTCTCATCTCCAGTACAGGAGGAGCTGGAAGAGTCCACCAAGCTTGTG 1078
241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
1079 GAGACCGCATCCAGTCTCCATGATGAGCCGCGAGGGGCTACCTCTCTCAAGTGCCAAG 1138
261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
1139 CAGCTCATCAAGAGCATTTAGAACCTCCAAAGGCTGCGAGCTGGGGAGACAGAGCAA 1198
281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
1199 GCCTTTGAGACATGGACTACTTACTCTGGACTTAGACACATAGCAGAGGCTTGAGG 1258
301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
1259 GCATTGACTTTGGGACA 1276
321 AlaIleAspPheGlyThr 326
RESULT 12
US-10-060-634C-46
; Sequence 46, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 46
; LENGTH: 351
; TYPE: PRT
; ORGANISM: rat
US-10-060-634C-46
Alignment Scores:
Pred. No.: 4.6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservatives: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 15 Gaps: 0
US-10-775-649-5 (1-1597) x US-10-060-634C-46 (1-351)
QY 299 ATGGATTATAATCTAGCTGATTCCTGATGAACGCTATGAGAACCTGAGAACGAG 358
Db 1 MetAspTyrLysSerGlyLeuLeuProAspGlyAsnAlaMetGluAsnLeuGluysGln 20
QY 359 CTGATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGCTCATCTGCTGCCCAA 418
Db 21 LeuileCysProileCysLeuGluMetPheThrLysProValIleLeuProCysGln 40
QY 419 CACAACCTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGGGTGGCTGAGTGCATGTCGTGAGTGCTGTTCCGTTGCTGCTGCTGCGCCCAT 538
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTGATCATGACCGCGGCGGTACGCGCTGCAGAGAACCTGCTGTGGAAAC 598
Db 81 GluValIleMeCaspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGGAGTGCTCCAGTCGGCCCTCGCAGAAAGCAGCCCGG 658
Db 101 IleileAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGGAACAGCAAGACAGAGATCAATCTACTGCTCACTGCTCAGGTGAGTGCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTGCAAGTGTTGGGCTCACCGGCTCACCGGCTGTGAGTTGCCCTTTGCA 778
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTCTTCAAGGACAGAAAGACTGAGCTGAGTAACCTGATCTCCATGCTGCTGGGGG 838
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGACAGCATCATCTCTCAGCTGGAGGACTCTGTGAGAGTACCAGGAG 898
Db 181 AsnAspArgValGlnThrIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGTGAAGGAGGCTGAGTACAGAGTTTGACACCTCTTACGCCATCTG 958
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
```

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 351
; TYPE: PRT
; ORGANISM: rat
; US-10-060-634C-47

Alignment Scores:
Pred. No.: 4,6e-121 Length: 351
Score: 1671.00 Matches: 319
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 97.85% Mismatches: 6
Query Match: 58.67% Indels: 0
DB: 15 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-060-634C-47 (1-351)

QY 299 ATGGATTATTAATCTAGCTGATTCCTGATGAAACGCTATGAGAACCTGGAGAACGAG 358
Db 1 MetAspTyrLysSerGlyLeuIleProAspGlyAsnAlaMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTCTGCTGGAGATGTTTACCAGCCTGTGTCATCTGCTCCCTGCCAA 418
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40
QY 419 CACAACTCTGCCGGAAGTGTGCCAACGACATCTTCCAGCTGCCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrTrpThr 60
QY 479 AACCGGTGGCTGCTGATGTCTCATGTCTGAGGTGCTTCCGTTGCCCTCGTCCGCCCAT 538
Db 61 AsnArgGlyGlySerValSerMetSerGlyGlyArgPheArgCysProSerCysArgHis 80
QY 539 GAAGTATCATGACCGCGCACGGGTGTACGCCCTGCAGAGAACCTGCTGGTGGAAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGGAGTGTCTCAGTCCGCCCCCTGCAGAAAGCAGCCACCCG 658
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGAACACAGAACGACGAGATCAATCACTACTCTACGTCTACGTGTGAGTGCCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTGTCTCTCTGCAAGGTGTTTGGGCTCACCGCCTGACAGCCTGTGAGTTCCTCCCTTGC 778
Db 141 ThrCysSerLeuCysLysValPheGlyAlaHisGlnAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAAAGGACAGAGACTGAGCTGAGTAACTGCACTCTCCATGCTGTGTGGCGGG 838
Db 161 SerIlePheGlnGlyGlnLysThrGluLeuSerAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCTGTGAGAGTGCACCAAGGAG 898
Db 181 AsnAspArgValGlnThrIleIleSerGlnLeuGluAspSerCysArgValThrLysGlu 200
QY 899 AATAGCCACCGTGAAGGAGGAGCTGAGTACAGAGTTTGACACCTCTACGCCATCCTG 958
Db 201 AsnSerHisGlnValLysGluLeuSerHisLysPheAspAlaLeuTyrAlaIleLeu 220
QY 959 GATGAGAAAGAGCGAGCTGCTGCGCGGATTCAGCAGGAGCAGGAGGAGAGCTGGGC 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuAsp 240
QY 1019 TTCATCGAGCTGTATCTCCTCAGTACAGGACGCTGGAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuIleLeuGlnTyrArgGluGlnLeuGluLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATCCAGTCCCTGGATGAGCCGCGAGGGGTACCTTCTCTCAAGTGCACAG 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuSerAlaLys 280
QY 1139 CAGCTCATCAAGACATGTGTAAGGCTTCAAGGGCTGCCAGCTGGGGAAGACAGACAA 1198
Db 281 ProLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCGTTTGACAACATGACTACTTACTCTGGACTTGAACACATACGAGCGCTTGAGG 1258
Db 301 GlyPheGluAsnMetAspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaIleAspPheGlyThr 326

RESULT 13
US-10-060-634C-47
; Sequence 47, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
```

```
QY 1139 CAGCTCATCAAGAGCATTTAGAACCTCCAAAGGGCTGCCAGCTGGGGAGAGACAGAGCAA 1198
Db 281 ProLeuIleLeSerIleValGluAlaSerIleGlyCysGlnLeuGlyThrGluGln 300
QY 1199 GGCTTTGAGAACATCGACTACTTTACTCTGGACTTTAGAACACATAGCAGAGGCTTTGAGG 1258
Db 301 GlyPheGluAsnMetCaspTyrPheThrLeuAsnLeuGluHisIleAlaGluAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaIleAspPheGlyThr 326
RESULT 14
US-10-094-749-2861
; Sequence 2861, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2861
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2861
Alignment Scores:
Pred. No.: 1,49e-116 Length: 353
Score: 1613.00 Matches: 305
Percent Similarity: 97.55% Conservative: 13
Best Local Similarity: 93.56% Mismatches: 8
Query Match: $6.64$ Indels: 0
DB: 15 Gaps: 0
US-10-775-649-5 (1-1597) x US-10-094-749-2861 (1-353)
QY 299 ATGGATTATTAATCTAGCCTGATTCCTGATGAAACGGCTATGGAGAACCTGGAGAACGAG 358
Db 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTGCCTGGAGATGTTTACAAAGCCTGTGGTCAATCTGCCCTGCCAAC 418
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACTCTCGCGGAGTGTCACACGACATCTCCAGGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAsnProTyrTrpThr 60
```

```
QY 479 AACCGCGTGGCTCAGTGTCCATGTCTGAGAGTCTGTTCCGTTGCGCCCTCGTGGCGCCAT 538
Db 61 SerArgGlySerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTGATCATGGACCGGACCGGGGTGTACGGCTCGCAGAGGAACCTGCTGTGTGAAAC 598
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTTGATCATCAAGCAGGAGTGCTCCAGTCCGGCCCCCTGCAGAAAGGACGCCACCG 658
Db 101 IleIleAspIleTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTCCAAGGACACAGAAAGACGAGAGATCAACATCTACTGTCTCAGCTGTGAGTGCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTTGCAAGGTGTTTGGGCTCACCAGGCTGTGAGGTGGCCCTTTGCAA 778
Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAAGGACAGAGACTGAGCTGAGTAACTGCATCTCCATGCTGTGTGGGGG 838
Db 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCTGTGAGAGTGACCAAGGAG 898
Db 181 AsnAspArgValGlnThrIleIleThrGlnLeuGluAspSerArgArgValThrLysGlu 200
QY 899 AATAGCCACCAAGGTGAAGGAGGCTGAGTCAGAGTTTGACACCTCTACGCCATCTCG 958
Db 201 AsnSerHisGlnValLysGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220
QY 959 GATGAGAAAGAGAGCGAGCTGCTGCAGCGGATCACGACGAGGACGAGAGAGCTGGGC 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGluGlnLysLysLeuSer 240
QY 1019 TTCATCGAGGCTCTGATCTCTCAGTACAGGAGAGCTGGAAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuIleGlnGlnTyrGlnGluGlnLeuAspLysSerThrLysLeuVal 260
QY 1079 GAGACCGCCATCCAGTCCCTCGATGAGCCCGGAGGGGTACCTCTCTCAAGTGCCAA 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAAGAGCATTTGTAGAAGCTCCCAAGGGCTGCAGCTGGGGAGACAGAGCAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GGCTTTGAGAACATGGACTACTTTACTCTGGACTTAGAACACATAGCAGAGGCTTTGAGG 1258
Db 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
Db 321 AlaIleAspPheGlyThr 326
RESULT 15
US-10-221-625-85
; Sequence 85, Application US/10221625
; Publication No. US20040033942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILIMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: MATHUR, Preete
; APPLICANT: SHAH, Purvi
```


Db 96 IleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsnIleIle 115
QY 605 GACATCTACAAGCAGAGTGTCTCCAGTCGGCCCTGCAGAAAGCAGCCACCCGATGTGC 664
Db 116 AspileTyrLysGlnGluCysSerArgProLeuGlnLysGlySerHisProMetCys 135
QY 665 AAGAACACGAGACGAGAGAGATCAACATCTACTGTCTCACGTGTGAGGTGCTTACTGC 724
Db 136 LysGluHisGluAspGluLysAsnAniIleTyrCysLeuThrCysGluValProThrCys 155
QY 725 TCCTTGTGCAAGGTGTTCGGGCTCACAGGCTGTGAGGTTCGCTTGTCAAGGATC 784
Db 156 SerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGlnSerVal 175
QY 785 TTCCAAGGACAGACAGTGTGAGTGTACTGTCTCTCCATCTCTGTCGGTGGGGGAAACGAC 844
Db 176 PheGlnGlyGlnLysThrGluLeuAsnAnCysIleSerMetLeuValAlaGlyAsnAsp 195
QY 845 CGAGTGCAGACCATCTCTCAGCTGAGGAGTCTGTGAGAGTGCACGAGGAGATAGC 904
Db 196 ArgValGlnThrIleIleThrGlnLeuGluAspSerArgValThrLysGluAsnSer 215
QY 905 CACCAAGTGAAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 964
Db 216 HisGlnValLysGlnGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeuAspGlu 235
QY 965 AAGAAAGAGCGAGTGTGTGAGCGGATCACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1024
Db 236 LysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnLysLysLeuSerPheIle 255
QY 1025 GAGGCTCTGATCTCTCAGTACAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAG 1084
Db 256 GluAlaLeuIleGlnGlnTyrGlnGlnLeuAspLysSerThrLysLeuValGluThr 275
QY 1085 GCCATCCAGTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1144
Db 276 AlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLysGlnLeu 295
QY 1145 ATCAAGAGCATTTGTAAGCCTTCAAGGCTGCCAGCTGGGAGACAGAGCAAGGCTTT 1204
Db 296 IleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGlnGlnGlyPhe 315
QY 1205 GAGAACATGAGTACTTTTACTTGTGACTTTAGAACACATAGCAGAGCCTTGTAGGCCATT 1264
Db 316 GluAsnMetAspPhePheThrLeuAspLeuGluHisIleAlaAspAlaLeuArgAlaIle 335
QY 1265 GACTTTGGGACA 1276
Db 336 AspPheGlyThr 339

RESULT 17
US-10-061-043A-48
; Sequence 48, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061, 043A
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338, 742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311, 697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264, 926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-061-043A-48
Alignment Scores:
Pred. No.: 1,78e-116 Length: 353
Score: 1612.00 Matches: 305
Percent Similarity: 97.24% Conservative: 12
Best Local Similarity: 99.56% Mismatches: 9
Query Match: 56.60% Indels: 0
DB: 14 Gaps: 0
US-10-775-649-5 (1-1597) x US-10-061-043A-48 (1-353)
QY 299 ATGGATTATAATCTAGGCTGATTCCTGATGAAACGGCTATGAGAACCTGGAGAACGAG 358
Db 1 MetAspTyrLysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTCCCATCTGCTCGAGATGTTTACCAAGCCTGTGGTCTCATCTGCTGCCCTGCCAA 418
Db 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeuProCysGln 40
QY 419 CACAACCTCTGCGGAGGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC 478
Db 41 HisAsnLeuCysArgLysCysAlaAsnAspilePheGlnAlaAsnProTyrTrpThr 60
QY 479 AACCCGGTGGCTAGTGTCCATGTCTGAGAGTCTGTTCCGTGGCCCTCGTCCGCCCAT 538
Db 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTGATCATGACCGCAGCGGGGTGACCGCTGCAGAGGAACTGCTGCTGGTGAACAC 598
Db 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGATCATCTACAAGCAGGAGTGTCCAGTCCGCGCCCTGCAGAAAGCAGCACCCG 658
Db 101 IleIleAspileTyrLysGlnGluCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTCGAAGGAAACAGAAAGACGAGAAGATCAACATCTACTGTCTCAGCTGTGAGTGCCT 718
Db 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTGTGCAAGGTGTTGGGGCTCACACGAGGCTGTGAGGTGCTCCCTTTGCAA 778
Db 141 ThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGluValAlaProLeuGln 160
QY 779 AGCATCTTCCAAAGGACAGAAAGTCAAGTGTGAGTGTGATCTCCATCTGCTGTGCGGGG 838
Db 161 SerValPheGlnGlyLysThrGluLeuAsnAnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACCATCTCTCAGCTGGAGGACTCTGTGAGAGTGCACCAAGGAG 898
Db 181 AsnAspArgValGlnThrIleTyrThrGlnLeuGluAspSerArgArgValThrLysGlu 200
QY 899 AATAGCCACAGGTGAAGGAGGCTGAGTCAAGAGTTTGACACCTCTACGCCATCTCCG 958
Db 201 AsnSerHisGlnValLysGluGluLeuSerGlnLysPheAspThrLeuTyrAlaIleLeu 220
QY 959 GATGAGAAAGAGAGCAGTGTCTGAGCGGATCACGACGAGGACGAGAGAGTGTGGGC 1018
Db 221 AspGluLysLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuSer 240
QY 1019 TTCATCGAGGTCTCATCTCTCCAGTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTG 1078
Db 241 PheIleGluAlaLeuIleGlnGlnTyrGlnGlnLeuAspLysSerThrLysLeuVal 260
QY 1079 GAGACCGCATCCAGTCTCTGAGTGCAGCGGAGGGGTACCTCTCTCAAGTGCACAAG 1138
Db 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAAGAGCATTTGTAGAAGCCTCCAAGGCTGCACAGTGGGAGGACAGAGCAA 1198
Db 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyLysThrGluGln 300
QY 1199 GCCTTTGAGAACATCGACTACTTTTACTGTGGAACATAGACATAGAGCGCTTGAGG 1258

```
||||| 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
||||| 1259 GCCATTGACTTTGGGACA 1276
||||| 321 AlaIleAspPheGlyThr 326

RESULT 18
US-10-060-634C-48
; Sequence 48, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-634C-48

Alignment Scores:
Pred. No.: 1.78e-116 Length: 353
Score: 1612.00 Matches: 305
Percent Similarity: 97.24% Conservative: 12
Best Local Similarity: 93.56% Mismatches: 9
Query Match: 56.60% Indels: 0
DB: 15 Gaps: 0

US-10-775-649-5 (1-1597) x US-10-060-634C-48 (1-353)

QY 299 ATGGATTATAAATCTAGCTGATTCCTGATGAAACGCTATGGAGAACCTGGAGAGCAG 358
DB 1 MetAspTyr-LysSerSerLeuIleGlnAspGlyAsnProMetGluAsnLeuGluLysGln 20
QY 359 CTGATCTGCCCATCTCCCTGGAGATGTTTACCAAGCCTGTGTCTACTCTGCCCTGCCAA 418
DB 21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40
QY 419 CACAACCTCTCGCGGAAGTGTGCCAACGACATCTCCAGGCTCGGAATCCCTACTGGACC 478
DB 41 HisAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaAlaAsnProTyrIleThr 60
QY 479 AACCGCGGTGGCTAGTGTCCATGTCTGGAGGTGTTTCCGTTGCCCTCGTGCCTGCCCAT 538
DB 61 SerArgGlySerSerValSerMetSerGlyGlyArgPheArgCysProThrCysArgHis 80
QY 539 GAAGTCAATCATGGACCGGACCGGGGTACGGCTCAGAGGAACTGCTGGTGGAAAC 598
DB 81 GluValIleMetAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuValGluAsn 100
QY 599 ATCATTGACATCTACAAGCAGGAGTCTCCAGTCGGCCCTCGCAGAAAGCAGCCACCG 658
DB 101 IleIleAspIleTyrLysGlnLysCysSerSerArgProLeuGlnLysGlySerHisPro 120
QY 659 ATGTGCAAGAAACGAGAACCGAAGATCAACATCTACTGTCTACGTGTGAGGTGCCT 718
DB 121 MetCysLysGluHisGluAspGluLysIleAsnIleTyrCysLeuThrCysGluValPro 140
QY 719 ACTTGCTCTCTGTGCAAGGTGTTTGGGCTCACCAGGCTGTGAGGTGCCCTTGGAA 778
DB 141 ThrCysSerMetCysLysValPheGlyIleHisAlaCysGluValAlaProLeuGln 160
```

```
QY 779 AGCATCTTCCAAGGACAGAAAGCTGAGCTGAGTAACCTGCATCTCCATCTGCTGGTGGCGGG 838
DB 161 SerValPheGlnGlyGlnLysThrGluLeuAsnAsnCysIleSerMetLeuValAlaGly 180
QY 839 AACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAG 898
DB 181 AsnAspArgValGlnThrIleTyrThrGlnLeuGluAspSerArgValThrLysGlu 200
QY 899 AATAGCCACCAAGTGAAGGAGGAGCTGAGTCAGAGTTTGCACACCTCTACGCCATCCTG 958
DB 201 AsnSerHisGlnValLysGluGluSerGlnLysPheAspThrLeuTyrAlaIleLeu 220
QY 959 GATGAGAAGAAGCAGGAGCTGCTGCAGCCGATCACCAGCAGGACAGAGAGAGCTGGGC 1018
DB 221 AspGluLysSerGluLeuLeuGlnArgIleThrGlnGlnGlnGluLysLeuSer 240
QY 1019 TTCATCGAGGCTCTGATCTCCAGTACAGGAGGAGCTGGAAGTCCACCAAGCTTGTG 1078
DB 241 PheIleGluAlaLeuIleGlnGlnTyrGlnGlnLeuAspLysSerThrLysLeuVal 260
QY 1079 GAGACCGCCATCCAGTCCCTCGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCAG 1138
DB 261 GluThrAlaIleGlnSerLeuAspGluProGlyGlyAlaThrPheLeuLeuThrAlaLys 280
QY 1139 CAGCTCATCAAGCAGCATCTAGAGCCTCCAAAGGCTGCCAGCTGGGGGAGACAGAGCAA 1198
DB 281 GlnLeuIleLysSerIleValGluAlaSerLysGlyCysGlnLeuGlyThrGluGln 300
QY 1199 GGCTTTGAGAACATGAGTACTTACTCTGGACTTAGAACACATACAGACGCGCTTGAGG 1258
DB 301 GlyPheGluAsnMetAspPheThrLeuAspLeuGluHisIleAlaAspAlaLeuArg 320
QY 1259 GCCATTGACTTTGGGACA 1276
DB 321 AlaIleAspPheGlyThr 326

RESULT 19
US-10-204-921-57
; Sequence 57, Application US/10204921
; Publication No. US20050095587A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PANZER, Scott R.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steven C.
; APPLICANT: SHAH, Purvi
; APPLICANT: CHALUP, Michael S.
; APPLICANT: CHANG, Simon C.
; APPLICANT: CHEN, Alice
; APPLICANT: D'SA, Steven A.
; APPLICANT: AMSHEY, Stefan
; APPLICANT: DAHL, Christopher R.
; APPLICANT: DAM, Tam C.
; APPLICANT: DANIELS, Susan E.
; APPLICANT: DUFOR, Gerard E.
; APPLICANT: FLORES, Vincent
; APPLICANT: FONG, Willy T.
; APPLICANT: GREENAWALT, Lila B.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Anissa L.
; APPLICANT: LIU, Tommy F.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: ROSEN, Bruce H.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: STOCKDREHER, Theresa K.
; APPLICANT: DAFFO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wensheng
```



```

Db      21  ValValIleLeuProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspIlePheGln  40
QY      458  GTTGGCAATCCCTACTGGACCAACCGCGTGGCTAGTGTCCATGCTCGAGGTGCTTTC  517
Db      41  AlaAlaAsnProTyrTrpThrSerArgGlySerSerValSerMetSerGlyArgPhe  60
QY      518  CGTTGCCCTCGTGGCCCATGAAGTGAATCATGGACCGCGCGGGGTGTACGGCCTGCAG  577
Db      61  ArgCysProThrCysArgHisGluValIleMetAspArgHisGlyValTyrGlyLeuGln  80
QY      578  AGAAGCTCTGGTGGAAACATCATATGATCTACAAGCAGGAGTGTCCAGTGGGCC  637
Db      81  ArgAsnLeuLeuValGluAsnIleIleAspIleTyrLysGlnGluCysSerSerArgPro  100
QY      638  CTGCAGAAAGGAGCCACCGATGTGCAAGGACACGAGACGAGAGATCAACATCTAC  697
Db      101  LeuGlnLysGlySerHisProMetCysLysGluHisGluAspGluLysIleAsnIleTyr  120
QY      698  TGTCTCACGTGTGAGGTGCTACTTCTCTTGTGTGCAAGGTGTTGGGGCTCACCAGGCC  757
Db      121  CysLeuThrCysGluValProThrCysSerMetCysLysValPheGlyIleHisLysAla  140
QY      758  TGTGAGGTGGCCCTTTGCAAGCATCTTCCAAGGACAGAGACTGAGCTGAGTAACTGC  817
Db      141  CysGluValAlaProLeuGlnSerValPheGlnGlyGlnLysThrGluLeuAsnAsnCys  160
QY      818  ATCTCCATCTGTGTGGCGGGAACGACCGAGTGCAGACCATCATCTCTCAGCTGGAGGAC  877
Db      161  IleSerMetLeuValAlaGlyAsnAspArgValGlnThrIleIleThrGlnLeuGluAsp  180
QY      878  TCGTCAGAGTGCACCAAGGAGAAATAGCCACCAAGGTGAAGGAGGAGCTGAGTCAGAAGTTT  937
Db      181  SerArgArgValThrLysGluAsnSerHisGlnValLysGluLeuSerGlnLysPhe  200
QY      938  GACACCTCTACGCCATCTCGATGAGAGAGAGAGAGAGAGCTGTCAGCGGATCAGCGAG  997
Db      201  AspThrLeuTyrAlaIleLeuAspGluLysLysSerGluLeuGlnArgIleThrGln  220
QY      998  GAGCAGGAGGAGAGCTGGGCTTCATCGAGGCTCTGATCCTCCAGTACAGGGAGCAGCTG  1057
Db      221  GluGlnGluLysLeuSerPheIleGluAlaLeuIleGlnGlnTyrGlnGlnLeu  240
QY      1058  GAAAGTCCACCAAGCTTGTGGAGACCGCATCCATCCCTGATGAGCCCGAGGGGCT  1117
Db      241  AspLysSerThrLysLeuValGluThrAlaIleGlnSerLeuAspGluProGlyGlyAla  260
QY      1118  ACCTTCCTCTCAAGTCCCAAGCAGCTCATCAGAGCATTTAGAGCCCTCCAGGGCTGC  1177
Db      261  ThrPheLeuLeuThrAlaLysGlnLeuIleLysSerIleValGluAlaSerLysGlyCys  280
QY      1178  CAGCTGGGAACAGACAGCAAGGCTTTGAGAATCATGGACTTACTTTACTCTGGACTTAGAA  1237
Db      281  GlnLeuGlyLysThrGlnGlnGlyPheGluAsnMetAspPhePheThrLeuAspLeuGlu  300
QY      1238  CACATAGCAGGCTTTGAGGGCCATTGACTTTGGGACA  1276
Db      301  HisIleAlaAspAlaLeuArgAlaIleAspPheGlyThr  313

```

Search completed: June 15, 2005, 15:09:10
Job time : 144 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2005, 08:10:59 ; Search time 840 Seconds
(without alignments)
11254.556 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 1597
Sequence: 1 ctcgagattacccttacag.....Gaaataaattatctcgtgcc 1597

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1597	100.0	1597	6	ABA99063 Murine mu
2	890.8	55.8	1053	6	ABQ79506 Rat MURF1
3	803.8	50.3	2097	6	ABQ79507 Human MUR
4	802.2	50.2	1231	5	AAH90037 Human bon
5	802.2	50.2	1764	5	ABA83058 Human tra
6	802.2	50.2	2700	12	ADQ24981 Human sof
7	800.6	50.1	1764	10	ADA53654 Human cod
8	797.4	49.9	1781	4	AAS25842 Human cdn
9	797.4	49.9	1781	8	ABX73183 Human nov
10	747.8	46.8	1757	6	ABS70380 Human bon
11	747.8	46.8	2110	5	AAS42490 Human cdn
12	679.8	42.6	1796	5	AAH89924 Human bon
13	674	42.2	1183	5	AAH90117 Human bon
14	547.4	34.3	630	6	ABQ79510 Human nov
15	484.6	30.3	1431	6	ABA99061 Murine mu
16	481.8	30.2	1405	10	ADC30183 Human nov
17	481.8	30.2	1913	5	AAH68563 Human pro
18	481.8	30.2	1390	4	AAH78026 Nucleotid
19	480.2	30.1	1349	3	AAA72433 Human nuc
20	444.4	27.8	867	6	ABQ79512 Human MUR

21	432.2	27.1	2590	6	ABA99062	AbA99062 Murine mu
22	430.6	27.0	1925	10	ADB62519	Abd62519 Human cdn
23	430.6	27.0	2434	8	AAH49597	Aad49597 Human cyt
24	430.6	27.0	2634	10	ADB62279	Adb62279 Human cdn
25	430.6	27.0	2662	12	ADO24315	Adq24315 Human sof
26	421.2	26.4	1762	4	AAS25855	Aas25855 Human cdn
27	421.2	26.4	1762	8	ABX73196	Abx73196 Human nov
28	412.2	25.8	1426	10	ADC30799	Adc30799 Human nov
29	390	24.4	531	3	AAC75285	Aac75285 Human ORF
30	390	24.4	531	6	ABN78104	Abn78104 Human int
31	374.2	23.4	1500	4	AAF27653	Aaf27653 DNA encod
32	329.4	20.6	2040	6	ABN85313	Abn85313 Human cyt
33	277	17.3	1039	6	ADA42866	Aad42866 Human DNA
34	277	17.3	1039	10	ACH62597	Ach62597 Human ven
35	260.6	16.3	424	9	ACH18104	Ach18104 Human adu
36	246.4	15.4	411	9	ACH17597	Ach17597 Human adu
37	244.2	15.3	446	4	AAS26303	Aas26303 Human cdn
38	244.2	15.3	446	8	ABX73644	Abx73644 Human nov
39	220.6	13.8	2762	12	ADP22641	Adp22641 Sea-squir
40	218.8	13.7	573	10	ADC32553	Adc32553 Human nov
41	217.8	13.6	587	4	AAS26314	Aas26314 Human cdn
42	217.8	13.6	587	8	ABX73655	Abx73655 Human nov
43	141.6	8.9	766	12	ADQ25137	Adq25137 Human sof
44	141.6	8.9	2000	11	ACN89140	Acn89140 Breast ca
45	123.4	7.7	475	12	ADQ21255	Adq21255 Human sof

ALIGNMENTS

RESULT 1
ABA99063
ID ABA99063 standard; DNA; 1597 BP.

XX ABA99063;

XX 15-JUL-2002 (first entry)

XX Murine muscle ring finger protein 3 (MURF-3) coding sequence.

KW Muscle ring finger; MURF-3; mouse; cardiant; microtubule;

KW intermediate filament; striated muscle; cardiac hypertrophy;

KW heart disease; gene; db.

OS Mus musculus.

FH Key Location/Qualifiers

FT CDS 299..1330

FT /*tag= a

FT /product= "MURF-3"

XX WO200206318-A2.

XX 24-JAN-2002.

XX 18-JUL-2001; 2001WO-US022896.

XX 18-JUL-2000; 2000US-0219020P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Olson EN, Spencer JA;

XX WPI; 2002-241506/29.

XX P-PSDB; ABB08277.

XX Novel muscle ring finger protein useful for drug screening, and for
diagnosing and treating diseases, particularly cardiomyopathies.

XX Claim 4; Page 131-133; 134pp; English.

XX The sequence encodes murine muscle ring finger protein 3 (MURF-3). The
invention relates to a purified muscle ring finger (MURF) protein,

CC selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the		Db	
CC invention are involved in microtubule and intermediate filament		Qy	
CC establishment of striated muscle cells and have cardiac activity. The		Db	
CC MURF proteins are useful for screening a candidate substance for MURF		Qy	
CC protein-binding activity, in a cell, cell-free system or in vivo, and its		Db	
CC effect on interaction of MURF with microtubules, homodimerisation of		Qy	
CC MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction		Db	
CC of MURF with intermediate filaments, e.g. desmin, vimentin and		Qy	
CC cytokeleton, and heterodimerisation of MURF. The screened compounds are		Db	
CC useful for treating and preventing cardiac hypertrophy and heart		Qy	
CC diseases. MURF proteins are useful as antigens to immunise animals for		Db	
CC the production of antibodies		Qy	
XX		Db	
SQ Sequence 1597 BP; 405 A; 404 C; 438 G; 350 T; 0 U; 0 Other;		Qy	
Query Match 100.0%; Score 1597; DB 6; Length 1597;		Db	
Best Local Similarity 100.0%; Pred. No. 0;		Qy	
Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Db	
Qy 1	CTCGAGATTACCTTACAGAACTGTTCGGAGCACCTTTCCCTTGGGAGCACACTCAG 60	781	CATCTTCCAAAGACAGAGAGAGCTGAGCTGAGTAACCTCATCTCCATGCTGGTGGCGGGAA 840
Db 1	CTCGAGATTACCTTACAGAACTGTTCGGAGCACCTTTCCCTTGGGAGCACACTCAG 60	841	CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGAGCTCGTCAGAGTGCACCAAGAGAA 900
Qy 61	GGACAGGAGCGGCAAGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCA 120	841	CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGAGCTCGTCAGAGTGCACCAAGAGAA 900
Db 61	GGACAGGAGCGGCAAGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCA 120	901	TAGCCACCAAGGTGAAGAGGAGCTGAGTCAGAAAGTTTGACACCTCTAGCCCATCTCTGGA 960
Qy 121	GCAGACCATGGATAACTTGGAAAGCACTGATCTGCCATCTGCTCAGATGATGTTTAC 180	901	TAGCCACCAAGGTGAAGAGGAGCTGAGTCAGAAAGTTTGACACCTCTAGCCCATCTCTGGA 960
Db 121	GCAGACCATGGATAACTTGGAAAGCACTGATCTGCCATCTGCTCAGATGATGTTTAC 180	961	TGAGAAAGAGCGAGCTCTCGAGCGGATCAGCGAGGAGAGGAGGAGGAGGAGCTGGCTT 1020
Qy 181	GAGCCTGTGGTCAATCTCCCTTGGCAGCAACCTGTGCGAGAAATGTGCGGGCCCCC 240	961	TGAGAAAGAGCGAGCTCTCGAGCGGATCAGCGAGGAGAGGAGGAGGAGGAGCTGGCTT 1020
Db 181	GAGCCTGTGGTCAATCTCCCTTGGCAGCAACCTGTGCGAGAAATGTGCGGGCCCCC 240	1021	CATCGAGGCTCTGATCCTCCAGTACAGGAGGAGCTGCGGAGGAGTCCCAAGGCTTGTGGA 1080
Qy 241	TTGGAGACAAAGACTTGGTGTGACGAGGTGGCAAGACAGTGCATATTCAAAGCAATAT 300	1081	GRCCGCTATCCAGTCCCTCGGATGAGCCCGAGGGGCTACTCTTCTCTCAAGTGCCTCAAGCA 1140
Db 241	TTGGAGACAAAGACTTGGTGTGACGAGGTGGCAAGACAGTGCATATTCAAAGCAATAT 300	1081	GRCCGCTATCCAGTCCCTCGGATGAGCCCGAGGGGCTACTCTTCTCTCAAGTGCCTCAAGCA 1140
Qy 301	GGATTATTAATCTAGCTGATCTCTGATGGAAACGCTATGGAGAACCTTGAGAGAGAGCT 360	1141	GCTCATCAAGAGCAATTGTAGAACCTTCCAAAGGCTGCCAGCTGGGAGAGACAGAGCAAG 1200
Db 301	GGATTATTAATCTAGCTGATCTCTGATGGAAACGCTATGGAGAACCTTGAGAGAGAGCT 360	1141	GCTCATCAAGAGCAATTGTAGAACCTTCCAAAGGCTGCCAGCTGGGAGAGACAGAGCAAG 1200
Qy 361	GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCATCTGCTGCCCTGCCAACA 420	1201	CTTTGAGAACATGGAGTACTTTACTCTGACCTTAGAACACATAGCAGAGGCTTTGAGGGC 1260
Db 361	GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTCATCTGCTGCCCTGCCAACA 420	1201	CTTTGAGAACATGGAGTACTTTACTCTGACCTTAGAACACATAGCAGAGGCTTTGAGGGC 1260
Qy 421	CAACCTCTGCGGAAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTTGGACCA 480	1261	CATTGACTTTGGGACAGGTAAAGGATGTGATGTTTACATGTTTGACCTTTGAAAGGAGCG 1320
Db 421	CAACCTCTGCGGAAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTTGGACCA 480	1261	CATTGACTTTGGGACAGGTAAAGGATGTGATGTTTACATGTTTGACCTTTGAAAGGAGCG 1320
Qy 481	CCGCGGTGGCTCAGTGTCCATGCTCGAGGTGCTTTCCGCTGTCGCGCCCATGA 540	1321	TTCCCTCTTCAAGTTCGAGGGGAACTGTTTAAAGGCTCAAATTTACACAGCAGTGTGTAC 1380
Db 481	CCGCGGTGGCTCAGTGTCCATGCTCGAGGTGCTTTCCGCTGTCGCGCCCATGA 540	1321	TTCCCTCTTCAAGTTCGAGGGGAACTGTTTAAAGGCTCAAATTTACACAGCAGTGTGTAC 1380
Qy 541	AGTGATCATGGACCGGCAAGGCTGTACGGCTGCGAGAGAACCTGCTGGTGGAAACAT 600	1381	AGGTCTCTCTATGGAGCCCTGACTGCTTTAGTAGTGTCTAAGTAGACCAAGCTGTCTGG 1440
Db 541	AGTGATCATGGACCGGCAAGGCTGTACGGCTGCGAGAGAACCTGCTGGTGGAAACAT 600	1381	AGGTCTCTCTATGGAGCCCTGACTGCTTTAGTAGTGTCTAAGTAGACCAAGCTGTCTGG 1440
Qy 601	CATTGACATCTAAGCAGAGGTGCTCCAGTCCGCCCCCTGCAGAAAGGAGGAGCCACCCGAT 660	1441	AACACATAGAGATCTATCTTGGCCATCTCTGCTTTCTTGAGGGATGAGATAAAGGAGCATGT 1500
Db 601	CATTGACATCTAAGCAGAGGTGCTCCAGTCCGCCCCCTGCAGAAAGGAGGAGCCACCCGAT 660	1441	AACACATAGAGATCTATCTTGGCCATCTCTGCTTTCTTGAGGGATGAGATAAAGGAGCATGT 1500
Qy 661	GTCCAGGAGACAGAGAGAGATCAACATCTACTGCTCTCAGTGTGAGGTGCTTAC 720	1501	GCCCAACATGCTGGCTCCACAGACAACTTTGTGTGATGATCCAGGGTCTGGGACAGTGCC 1560
Db 661	GTCCAGGAGACAGAGAGAGATCAACATCTACTGCTCTCAGTGTGAGGTGCTTAC 720	1501	GCCCAACATGCTGGCTCCACAGACAACTTTGTGTGATGATCCAGGGTCTGGGACAGTGCC 1560
Qy 721	TTGCTCTTGTGCAAGGTGTTTGGGGCTCACAGGCTGTGAGGTGCTGAGGTTGCCCTTTGCAAG 780	1561	TGGTACATAAATGTTTTCGAAATAAATATCTCGTGCC 1597
Db 721	TTGCTCTTGTGCAAGGTGTTTGGGGCTCACAGGCTGTGAGGTGCTGAGGTTGCCCTTTGCAAG 780	1561	TGGTACATAAATGTTTTCGAAATAAATATCTCGTGCC 1597
Qy 781	CATCTTCCAAAGACAGAGACTGAGTGAATCTGATCTCCATGCTGGTGGCGGGAA 840		

RESULT 2
ABQ79506
ID ABQ79506 standard; DNA; 1053 BP.
XX
AC ABQ79506;
XX
AC
XX
DT 05-NOV-2002 (first entry)
XX
DE Rat MURF1 protein encoding DNA.
XX
KW Muscle atrophy protein; MURF1; MURF3; MAFBX; atrophy; neuroprotective;
XX Gene therapy; transgenic; gene; rat; ds.
XX Rattus sp.
FH Key
FT CDS
FT Location/Qualifiers
1..1053
/*tag= a

992	Db	GAGCAGCTAGGCGTGGCTCTCATTCCTTCCCA CAGAA TGGATTATAAGTCGAGCCTGAT	1051
322	Qy	TCCTGATGGAAACGCTATGGAGAACCTGGAGAACAGCTGATCTGCGCCCATCTGCGCTGGGA	381
1052	Db	CCAGGATGGGAAATCCCATGGAGAACTTGGAGAACAGCTGATCTGCGCTTATCTGCGCTGGA	1111
382	Qy	GATGTTTACCAAGCCTGTGTCATCTGCGCCTGCGCAACACAACTCTGCGCGGAAGTGTGC	441
1112	Db	GATGTTTACCAAGCAGTGGTTCATCTTGGCGGTGCGACACAACTGTGTGCGCGGAAGTGTGC	1171
442	Qy	CAACGACATCTTCCAGAGCTGGAAATCCCTACTGTGACCAACCGCGGTGGCTCAGTGTCCAT	501
1172	Db	CAATGACATCTTCCAGGCTGGAAATCCCTACTGTGACCAACCGCGGAGCTCAGTGTCCAT	1231
502	Qy	GTCTGGAGGTCTGTTCCGCTTGCCTCGTGGCGCCATGAAGTGATCATGTGACCGGACCGG	561
1232	Db	GTCTGGAGGCGTTTCCGCTGCCCCACTTGC CGCCACAGAGTGATCATGATCGTCAAGG	1291
562	Qy	GGTGTA CGGCTTG CAGAGGAACCTGCTGGTGGGAAAA CATATTGACATCTTACAAGCAGGA	621
1292	Db	AGTGTA CGGCTTG CAGAGGAACCTGCTGGTGGGAAAA CATCATGACATCTTACAAA CAGGA	1351
622	Qy	GTGCTCCAGTGGGCCCTG CAGAAAGCAGCCACCGATGTGCNAGGAA CACGAGACGA	681
1352	Db	GTGCTCCAGTGGGCCCTG CAGAAAGGCGAGTCACCCCATGTGCAAGGAGCAGCAAGATGA	1411
682	Qy	GAAGATCAA CATCTACTGTCTCAGCTGTGAGGTGCCCTTACTTGTCTCTTGTGCAAGGTGT	741
1412	Db	GAATAATCAA CATCTACTGTCTCAGCTGTGAGGTGCCCTTACTTGTCTCTTGTGCAAGGTGT	1471
742	Qy	TGGGGCTCA CCAAGCCTGTGAGGTGGCCCTTTG CAAAAGCATCTTCCAAGCAGCAAGAC	801
1472	Db	TGGGATCCACAAGCCTGCGAGGTGGCCCATTTG CAGAGTGTCTTCCAGGGA CAAAAGAC	1531
802	Qy	TGAGCTGAGTAA CTGCACTCTCCATCTGCTGGTGGGGGGAACGACCGAGTCGACAGCATCAT	861
1532	Db	TGAACTGAATTAAC TGTATCTCCATCTGCTGGTGGGGGGAATGACCGTGTG CAGACCATCAT	1591
862	Qy	CTCTCAGCTGGAGACTCTGTGCAGAGTGACCAAGAGGAATAGCCACACAGAGTGAAGGAGGA	921
1592	Db	CAC T CAGCTGGAGATTTCCCGT CGAGTGACCAAGAGGAACNGTCAC CAGGTTAAAGGAAGA	1651
922	Qy	GCTGAGTCAGAAGTTGACACCCCTCTACGCCATCCTGGATGAGAAAGAGCGAGCTGCT	981
1652	Db	GCTGAGCCAGAAGTTTGACACGTTGTATGCCATCTCTGGATGAGAAAGAAAGTGAAGTTGCT	1711
982	Qy	GCAGCGATCA CGCAGAGCAGGAGGAGAGAGCTGGCTTCA TCGAGGCTCTGATCTCTCCA	1041
1712	Db	GCAGCGATCA CGCAGGAGCAGGAGAGAAAGCTTAGCTTCA TCGAGGCCCTCA TCCAAGCA	1771
1042	Qy	GTACAGGGAGCAGCTGGAAGAGTCCACCAAGCTTGTGAGACCGCCATCAGTCCCTGGA	1101
1772	Db	GTA CCAAGAGCAGCTGGACAAGTCCA AAGCTGGTGGAACTGCCATCAGTCCCTGGA	1831
1102	Qy	TGAGCCGGAGGGGCTACCTTCTCTCAAGTGCCAAGCAGCTCATCAAGAGCATTTGTAGA	1161
1832	Db	CGAGCTGGGGAGGCCACTTCTCTTGA CTGCCAAGCAACTCATCAAAGCATTTGTGGA	1891
1162	Qy	AGCCTCCAAGGCTGCCAGCTGGGGAGACAGAGCAAGGCTTTGAGAA CATTGACTACTT	1221
1892	Db	AGCTTCCAAGGCTGCCAGCTGGGGAGACAGAGCAGGGCTTTGAGAA CATTGACTACTT	1951
1222	Qy	TACTCTGACTTAGAACACATAGCAGAGGCTTTCAGGGCCATTGACTTTGGGACAGGTAA	1281
1952	Db	TACTTTGGATTTAGACACATAGCAGACGCCCTGAGAGCCATTGACTTTGGGACAGATGA	2011
1282	Qy	AGGATGTGATG 1292	
2012	Db	GGAAGAGGAAG 2022	
RESULT 7			
ADAS3654			

Db 400 AGTTTACGGCCTGCAGAGGAACCTGCTGTGGAGAAACATCATCGACATCTCAAAAACGGA 459
QY 622 GTGCTCCAGTCGGCCCTGCAGAAAGCCAGCCAGCTGTGCAAGGACACGAAACGA 581
Db 460 GTGCTCCAGTCGGCCCTGCAGAAAGGCGATCACCCCATGTGCAAGGACGACGAAGATGA 519
QY 682 GAAGATCAACATCTACTGTCTCACTGTGTGAGGTGCGCTACTTGTCTCTTGTGCAAGGTGTT 741
Db 520 GAAATCAACATCTACTGTCTCACTGTGTGAGGTGCGCTACTTGTCTCTTGTGCAAGGTGTT 579
QY 742 TGGGGCTCACAGGCTGTGAGGTGCCCTTTGCAAGGACATCTTCCAAGGACAGAAGAC 801
Db 580 TGGGATCCACAGGCTGTGAGGTGCCCTTTGCAAGGACATCTTCCAAGGACAGAAGAC 639
QY 802 TGAGCTGAGTNACTGATCTCCATGTGTGTGGGGGAACGACCGAGTGCAGACGATCAT 861
Db 640 TGAATCGAATACTGTATCTCCATGTGTGTGGGGGAATGACCGTGTGCAGACCATCAT 699
QY 862 CTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGAAATAGCCACAGTGAAGGAGGA 921
Db 700 CACTCAGCTGGAGGATCCCGTCCAGTGACCAAGGAGAACAGTCCACAGGTAAGGAAGA 759
QY 922 GCTGAGTCAGAGTTTGACACCTCTTACGCGCATCTTGGATGAGAAAGAGCGAGCTGCT 981
Db 760 GCTGAGCCAGAGTTTGACACGTTGTATGCCATCTCGATGAGAGAAAGTGAGTTGCT 819
QY 982 GCAGCGGATCACGAGGACGAGGAGAGCTGGGCTTCATCGAGGCTGTGATCCTCCA 1041
Db 820 GCAGCGGATCACGAGGACGAGGAGAGCTGGGCTTCATCGAGGCTTCATCGAGGCTTCATCAGCA 879
QY 1042 GTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTTGTGGAGACCGCCATCCAGTCCCTGGA 1101
Db 880 GTACAGGAGCAGCTGGACAAGTCCACAAGCTGTTGGAACATGCCATCCAGTCCCTGGA 939
QY 1102 TGAGCCGAGGGGCTACCTTCTCTCAAGTGCACCAAGCGCTCATCAAGAGCATTTAGA 1161
Db 940 CGAGCCTGGGGAGCCACCTTCTCTTGACTGCAAGCAACTCATCAAAAGCATTTGGA 999
QY 1162 AGCTCCAGGGCTGCAGCTGGGAGACAGAGCGCTTTGAGAACATGGACTACTT 1221
Db 1000 AGCTTCAAGGGCTGCAGCTGGGAGACAGAGCGCTTTGAGAACATGGACTACTT 1059
QY 1222 TACTTGGACTTAGAACACATAGCAGAGCGCTTTGAGGGCCATTTGCTTTGGGACAGGTA 1281
Db 1060 TACTTTGGATTTAGACACATAGCAGAGCGCTTTGAGAGCCATTTGACTTTTGGGACAGATGA 1119
QY 1282 AGGATGTGATG 1292
Db 1120 GGAAGAGGAAG 1130

RESULT 8
AAS25842
ID AAS25842 standard; cDNA; 1781 BP.
XX
AC AAS25842;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human cDNA encoding a novel secreted protein, Seq ID 21.
XX
KW Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;
KW cardiac; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virocid; fungicide; ophthalmological; vulnerary;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
XX preservative; antiproliferative.
OS Homo sapiens.
XX

PN WO200155322-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001341.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 25-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239837P.
PR 13-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246529P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-488783/53.
DR P-PSDB; AAU15855.
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Claim 1; SEQ ID NO 21; 980pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunoassays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
Query Match 49.9%; Score 797.4; DB 4; Length 1781;
Beat Local Similarity 85.8%; Pred. NO. 5.1e-203;
Matches 885; Conservative 0; Mismatches 146; Indels 0; Gaps 0;
QY 262 GACGAGGTGGGCAAGACAGTCGCATTTCAAAGCAATATGATTAATAATCTAGCTGAT 321
DB 82 GAGGAGCTAGGCTGGCTCTCATCTTCCACAGATGATTAATAGTCAGGCTGAT 141
QY 322 TCCTGATGAAACGCTATGGAGAACCTGGAGAGCAGTGTCTGCCCATCTGCTCGA 381
DB 142 CCAGGATGGGAATCCCATGGAGAACTTGGAGAGCAGTGTCTGCCCTATCTGCTCGA 201
QY 382 GATGTTTACCAAGCCTGTGGTTCATCTGCTGCTGCCAACACACCTCTGCCGGAAGTGC 441
DB 202 GATGTTTACCAAGCCAGTGGTTCATCTGCTGCTGCCAGCACCACTGTGCCGGAAGTGC 261
QY 442 CAAGCACATCTTCCAGGCTGGGAATCCCTACTGGACCAACCGCGTGGCTCAGTGTCCAT 501
DB 262 CAATGACATCTTCCAGGCTGCAATCCCTACTTGGACACGCGGCGCAGCTCAGTGTCCAT 321
QY 502 GTCTGGAGGTGTTTCCGTTTCCGCTGCTGCCCATGAAGTGATCATGGACCGGCACGG 561
DB 322 GTCTGGAGGCGTTTCCGCTGCTGCCCATGCCACGCGGCGGAGTATCATGGATCGTCA 381
QY 562 GGTGTACGGCTGACAGGAACCTGCTGGTGGAAACATCAATTGACATCTACACAGCA 621
DB 382 AGTTTACGGCTGACAGGAACCTGCTGGTGGAGAACATCATCGACATCTACAAACAGCA 441
QY 622 GTGCTCCAGTGGCGGCTGCAAGAGGCGAGCCACCGCATGTGCAAGGAACACAGAGCA 681
DB 442 GTGCTCCAGTGGCGGCTGCAAGAGGCGAGTACCCTCATGTGCAAGGACACAGAGATGA 501
QY 682 GAAGATCAACATCTACTGTCTCAGCTGTGAGTGCTACTTGTCTCTTGTGCAAGGTGT 741
DB 502 GAAAAATACATCTACTGTCTCAGCTGTGAGTGCTGCCACCTGCTCATGTGCAAGGTGT 561
QY 742 TGGGGCTCACGAGGCTGTGAGGTGGCCCTTTGCAAGAGCATCTTCCAGGACAGAGAC 801
|||||

Db 562 TGGATCCACAAGCCCTGCGAGGTGGCCCCATTGCGAGAGTGTCTTCCAGGGACAAAAGAC 621
QY 802 TGAGCTCAGTAACCTGCAATCTCCATCTGCTGGTGGCGGGAACGACCGAGTGCAGACGATCAT 861
Db 622 TGAACCTAATATGTATCTCCATCTGCTGGTGGCGGGAATGACCGTGTGCGAGACCATCAT 681
QY 862 CTCTCAGCTGGAGGACTCTGTCAGAGTGACCAAGGAGAAATAGCCACAAGGTGAAGGAGGA 921
Db 682 CACTCAGCTGGAGGATTCCTCGTCCAGTGACCAAGGAGAACAGTCCACCGTAAAGGAAGA 741
QY 922 GCTGAGTCAGAGTTTGAACACCTCTACGCCATCTCGGATGAGAAAGAGCGAGTGTCT 981
Db 742 GCTGAGCCAGAGTTTGAACACGTGTGATGCCATCTCGGATGAGAAAGAGTGTGTCT 801
QY 982 GCAGCCGATCACGACGAGCAGGAGCAGAGGAGGAGCTGGGCTTCATCGAGGCTCTGATCCTCCA 1041
Db 802 GCAGCCGATCACGACGAGCAGGAGCAGAGGAGGAGGCTTAGCTTCATCGAGGCCCTCATCCAGCA 861
QY 1042 GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTTGAGAGACCGCCATCCAGTCCCTGGA 1101
Db 862 GTACAGGAGCAGCTGGACAAGTCCACAAGCTGGTGGAAACTGCCATCCAGTCCCTGGA 921
QY 1102 TGAGCCCGGAGGGCTACCTTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATTTGAGA 1161
Db 922 CGAGCTGGGGAGCCACCTTCTCTTGACTGCGCAAGCAACTCATCAAAAGCATTTGGA 981
QY 1162 AGCTCCAAAGGGCTGCAGCTGGGGAAGCAGAGCAAGGCTTTGAGAACATGGACTACTT 1221
Db 982 AGTTCNAGGGTGCAGCTGGGGAAGCAGAGCAGGCTTTGAGAACATGGACTACTT 1041
QY 1222 TACTCTGGACTTAGAACACATAGCAGGCTTTGAGGGCCATTTGACTTTGGGACAGGTAA 1281
Db 1042 TACTTTGGATTTAGAGCACATAGCAGACGCGCTTGAGAGCATTGACTTTGGGACAGATGA 1101
QY 1282 AGCATGTATG 1292
Db 1102 GGAAGAGGAAG 1112
RESULT 9
ABX73183
ID ABX73183 standard; DNA; 1781 BP.
XX AC ABX73183;
XX DT 18-MAR-2003 (first entry)
XX DE Human novel polynucleotide #11.
KW Human; gene; db; neural disorder; immune system disorder; renal disorder;
KW muscular disorder; respiratory disease; reproductive disorder;
KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
KW hyperproliferative disorder; inflammatory disease; allergic reaction;
KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
KW cardiovascular; nephrotropic; cytostatic; antiatherogenic; thrombolytic;
KW haemostatic; antiarteriosclerotic.
XX OS Homo sapiens.
XX PN US2002132753-A1.
XX PD 19-SEP-2002.
XX PF 17-JAN-2001; 2001US-00764864.
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 07-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
XX PR 11-JUL-2000; 2000US-0217496P.
XX PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0228688P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX PI Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-147444/14.
DR P-PSDB; ABU54923.
XX New polypeptides and nucleic acids, useful in gene therapy for treating,
PT inhibiting or preventing e.g. neural, immune system, muscular,
PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
PT renal disorders.
XX Claim 1; SEQ ID NO 21; 402pp; English.
PS The invention relates to human novel polypeptides and their associated
XX polynucleotides. The polypeptides and polynucleotides are useful in gene
CC therapy for treating, inhibiting or preventing neural disorders, immune
CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders,
CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent

CC human novel polynucleotides of the invention		
XX	Sequence 1781 BP; 494 A; 399 C; 511 G; 377 T; 0 U; 0 Other;	
Query Match 49.9%; Score 797.4; DB 8; Length 1781;		
Best Local Similarity 85.8%; Pred. No. 5.1e-202;		
Matches 885; Conservative 0; Mismatches 146; Indels 0; Gaps 0;		
QY	262 GACGAGGTGGGCAAGACAGATCGCATTTTCAAAAGCAATATGGATTATAAATCTAGCCTGAT	321
DB	1102 TACTTTGGATTAGACACATAGCAGACCCCTGAGGCCATTGACTTTGGACAGATGA	1101
QY	82 GAGCAGCTAGCGGTGCTCTATTCTTCCACAGAAATGGATTATAAGTCGAGCCTGAT	141
DB	1282 AGGATGTGATG 1292	
QY	322 TCCTGATGAAACGCTATGAGAAACCTGGAGAGAGCTGATCGCCCATCTGCTGGA	381
DB	1102 GGAAGAGGAG 1112	
QY	142 CCAGGATGGGAATCCCATGGAGAACTTGAGAGAGCAGCTGATCGCCCTATCTGCTGGA	201
DB		
QY	382 GATGTTTACCAAGCCTGTGCTCATCTGCGCCGCAACACACACCTCTGCGGAAGTGTC	441
DB		
QY	202 GATGTTTACCAAGCAGTGTGTCATCTGCGGTGCCAGCAACCTTGCCGGAAGTGTC	261
DB		
QY	442 CAACGACATCTTCCAGGCTCGAAATCCCTACTGACCAACCGCGGTGGCTCAGTGTCCAT	501
DB		
QY	262 CAATGACATCTTCCAGGCTGCAATCCCTACTGACCAACCGCGGTGGCTCAGTGTCCAT	321
DB		
QY	502 GTCTGAGGTGCTTCCGTTGCCCTCTGCGCCCATGAAAGTATCATGGACCGGACGCG	561
DB		
QY	322 GTCTGAGGCGCTTTCGCTGCCCACTCTGCCCAACGAGGTGATCATGGATCGTCAAGG	381
DB		
QY	562 GTGTACGCGCTGACAGAGAACTCTGCTGTGGAACATCATTTGACATCTACAACAGCA	621
DB		
QY	382 AGTTTACGCGCTGACAGAGAACTCTGCTGTGGAACATCATTTGACATCTACAACAGCA	441
DB		
QY	622 GTGCTCCAGTGGCGCCCTGACAGAAAGGACGACCCGATGTGCAAGGAACACGAAGCA	681
DB		
QY	442 GTGCTCCAGTGGCGCCCTGACAGAGGAGTCAACCCATGTGCAAGGAACACGAAGTGA	501
DB		
QY	682 GAAATCAACATCTACTGTCTCAGTGTGAGTGTCTTCTGCTCTTGTGCAAGGTGT	741
DB		
QY	502 GAAAAATAACTACTGTCTCAGTGTGAGTGTCTTCTGCTCTTGTGCAAGGTGT	561
DB		
QY	742 TGGGCTCACAGGCTGTGAGGTGCGCTTTCGCAAGCATCTTCCAGGACACAGAC	801
DB		
QY	562 TGGGATCCAAGGCTGTGAGGTGCGCTTTCGCAAGCATCTTCCAGGACACAGAC	621
DB		
QY	802 TGAGCTGAGTAACTGATCTCCATGTGCTGGGGAACGACCGAGTGCAGACCATCAT	861
DB		
QY	622 TGAATCTGATATCTGATCTCCATGTGCTGGGGAACGACCGAGTGCAGACCATCAT	681
DB		
QY	862 CTCTCAGCTGGAGGACTCTGTGAGAGTGAACCAAGAGAAATAGCCACGAGTGAAGGA	921
DB		
QY	682 CACTCAGCTGGAGGATTCCTGCTGAGTGAACCAAGAGAACTGACCAAGTAAAGGA	741
DB		
QY	922 GCTGATCAGAGTGTGACACCTCTACCCATCTGATGAGAGAGAGAGAGAGTCTCT	981
DB		
QY	742 GCTGAGCCAGAGTGTGACACCTGTGATGCTGATGAGAGAGAGAGAGTGTCTCT	801
DB		
QY	982 GCAGCGGATCAGCAGGAGCAGAGAGAGAGTGGCTTTCATCGAGGCTCTCATCTCCA	1041
DB		
QY	802 GCAGCGGATCAGCAGGAGCAGAGAGAGAGTGTGAGAGAGAGAGTGTCTCTCAT	861
DB		
QY	1042 GTACAGGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGTGTCTCTCAT	1101
DB		
QY	862 GTACAGGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGTGTCTCTCAT	921
DB		
QY	1102 TGAGCCGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGTGTCTCTCAT	1161
DB		
QY	922 CGAGCCTGAGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGTGTCTCTCAT	981
DB		
QY	1162 AGCCTTCAAGGCTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGTGTCTCT	1221
DB		
QY	982 AGCCTTCAAGGCTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGTGTCTCT	1041
DB		
QY	1222 TACTCTGGAATTAGAACACATAGAGAGGCGCTTGGAGGCCATTGACTTTGGGACAGGTA	1281

DB	1042 TACTTTGGATTAGACACATAGCAGACCCCTGAGGCCATTGACTTTGGACAGATGA	1101
QY	1282 AGGATGTGATG 1292	
DB	1102 GGAAGAGGAG 1112	
RESULT 10		
ABS70380		
ID	ABS70380 standard; cDNA; 1757 BP.	
XX		
AC	ABS70380;	
DT	27-NOV-2002 (first entry)	
XX		
DB	Human bone remodelling gene #37.	
XX		
KW	Bone remodelling; osteoporosis; human; gene; ss.	
OS	Homo sapiens.	
XX		
PN	US6426186-B1.	
XX		
PD	30-JUL-2002.	
XX		
PF	18-JAN-2000; 2000US-00484970.	
XX		
PR	18-JAN-2000; 2000US-00484970.	
XX		
PA	(INCY-) INCYTE GENOMICS INC.	
XX		
PI	Jones KA, Volkmut W, Walker MG;	
XX		
DR	WPI: 2002-673014/72.	
DR	P-PSDB; ABG93804.	
XX		
PT	A combination of polynucleotides which are co-expressed with genes known to be involved in bone remodeling and osteoporosis are useful in an array for the diagnosis of bone remodeling and osteoporosis associated disorders.	
PS	Claim 1; Col 135-138; 206pp; English.	
CC	The invention relates to a combination comprising a number of substantially purified and isolated polynucleotides which are co-expressed with genes known to be involved in bone remodeling and osteoporosis. The invention is used to diagnose disorders associated with bone remodeling or osteoporosis. ABS70344-ABS70512 represent human bone remodelling genes of the invention	
QY	Sequence 1757 BP; 473 A; 388 C; 513 G; 383 T; 0 U; 0 Other;	
Query Match 46.8%; Score 747.8; DB 6; Length 1757;		
Best Local Similarity 82.8%; Pred. No. 8.8e-189;		
Matches 854; Conservative 0; Mismatches 177; Indels 0; Gaps 0;		
QY	262 GACGAGGTGGGCAAGACAGATCGCATTTTCAAAAGCAATATGGATTATAAATCTAGCCTGAT	321
DB	88 GAGGAGCTAGCGGTGGCTCTCATCTTCCACAGATGGATTATAGTCGAGCCTGAT	147
QY	322 TCCTGATGGAACGCTATGAGAACTTGGAGAACCTGGAGAGCAGCTGATCTGCCCATCTGCTGGA	381
DB	148 CCAGGATGGGAATCCATGGAGAACTTGGAGAAAGCAGCTGATCTGCCCTATCTGCTGGA	207
QY	382 GATGTTTACCAAGCCTGTGCTCATCTGCGCCGCAACACACCTCTGCCGGAAGTGTC	441
DB	208 GATGTTTACCAAGCAGTGTGCTCATCTTGGCGTGGCAGCAACACCTGTGCCGGAAGTGTC	267
QY	442 CAACGACATCTTCCAGGCTGGGAATCCCTACTGGAACCAACCGCGTGGCTCAGTGTCCAT	501
DB	268 CAATGATATTTTCCAGGCTCTAACCCGTATTTGGCCCAAGAGGAGGTACCAACCATGGC	327

Db 328 ATCAGGGGCGCATTCCTCGCTGCCATCCTGTAGACATGAAGTGGTTTTGGATAGACATGG 387
Qy 562 GGTGTACGGCTGACAGAGAACTCTCTGTGTGAAACATCATTTGACATCTACAAGCAGGA 621
Db 388 GGTATATGACTTCAGAGGAACCTCTGTGTGAGAAACATCATCGACATCTACAACAGGA 447
Qy 622 GTGCTCCAGTCGGCCCTGACAGAAAGGAGCCACCGGATGTGCAAGAACACGAGAGGA 681
Db 448 GTGCTCCAGTCGGCCCTGACAGAAAGGAGCTCACCCCATGTGCAAGAGGACGAAAGATGA 507
Qy 682 GAAAGTCAACATCTACTGTCTCACGTGTGAGGTGCTACTTGTCTTGTGCAAGGTGTT 741
Db 508 GAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCACTGCTCATGTGTGCAAGGTGTT 567
Qy 742 TGGGGCTCACAGGCTGTGAGGTGTCCTTTGCAAAAGCATCTTCCAAGGACAGAAAGAC 801
Db 568 TGGGATCCACAAGGCTGCGAGGTGSCCCATTGACAGAGTGTCTCCAGGGACAAAAGAC 627
Qy 802 TGAGCTGAGTAAGTATCTCATCTCTGCTGTGCGGGGAGACCGAGTGCAGACATCAT 861
Db 628 TGAATCTGAATAACTGTATCTCCATGCTGTGTGCGGGGAATGACCGGTGTGCAGACCATCAT 687
Qy 862 CTCTCAGCTGGAGGACTCTGTGAGAGTGACCAAGGAGAAATAGCCACAGGTGAAGGAGGA 921
Db 688 CACTCAGCTGGAGGATTCCTGTGAGTGACCAAGGAGAAAGTCAACAGGTAAAGGAAGA 747
Qy 922 GCTGAGTCAGAAAGTTTGACACCTCTTACGCCATCTCTGGATGAGAAAGAGAGCGAGTGT 981
Db 748 GCTGAGCCAGAAAGTTTGACACCTGTGTATGCCATCTCTGGATGAGAAAGTGAAGTGTCT 807
Qy 982 GCAGGGATCAGCAGGAGCAGGAGAGAGCTGGCTTTCATCGAGGCTCTGATCTCTCA 1041
Db 808 GCAGGGATCAGCAGGAGCAGGAGAGAAAGTGTAGCTTTCATCGAGGCTCTCATCCAGCA 867
Qy 1042 GTACAGGAGCAGCTGGAAGAGTCCACCAAGCTTGTGGAGACCGCATCCAGTCCCTGGA 1101
Db 868 GTACAGGAGCAGCTGGAAGAGTCCACCAAGCTTGTGGAACTGCCATCCAGTCCCTGGA 927
Qy 1102 TGAGCCGAGGAGGCTTACCTCTCTCAAGTCCCAAGCAGCTCATCAAGAGCATTTGTAGA 1161
Db 928 CGAGCCTGGGGAGCCACCTCTCTCTGTAGTCCCAAGCAACTCATCAAAAGCATTTGTGA 987
Qy 1162 AGCCTCCAGGCTGCGAGCTGGGAGAGACAGACAGCAGGCTTTGAGACATGGACTACTT 1221
Db 988 AGCTTCCAGGCTGCGAGCTGGGAGAGACAGACAGGAGGCTTTGAGAACATGGACTTCTT 1047
Qy 1222 TACTCTGAGCTTAGAACACATAGCAGAGGCTTTGAGGCGCATTTGAGGAGAGGTA 1281
Db 1048 TACTTTGGATTAGAGACATAGCAGAGGCTTGGAGGCGCATTTGAGGAGGAGATGA 1107
Qy 1282 AGGATGTGATG 1292
Db 1108 GGAAGGGAAG 1118
RESULT 12
AAH89924
ID AAH89924 standard; cDNA; 1796 BP.
AC AAH89924;
XX
XX 01-OCT-2001 (first entry)
XX Human bone marrow cDNA, SEQ ID NO: 55.
DE
DE Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
KW immunosuppressive; gene therapy; cytokine cell proliferation;
KW cell differentiation modulator; immune disorder; infection; cancer;
KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.
OS Homo sapiens.
XX

PN WO200153453-A2.
XX
PD 26-JUL-2001.
XX
PF 23-DEC-2000; 2000WO-US034960.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 30-NOV-2000; 2000US-0250583P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
PI Ren F, Wang J, Wethman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Drmanac RT;
XX
DR WPI: 2001-488707/53.
DR P-PSDB; AA00805.
XX
PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful for
PT treating e.g. cancer and immune deficiency disorders.
XX
PS Claim 1; Page 243-244; 648pp; English.
XX
CC The present sequence is one of 251 novel human polynucleotides expressed
CC in the bone marrow. The polynucleotide and the polypeptide encoded by it
CC are useful in the treatment of various immune deficiencies and disorders.
CC The deficiencies and disorders may be genetic, may be caused by a viral
CC (e.g. HIV), bacterial or fungal infection, or may result from an
CC autoimmune disorder, a coagulation disorder (e.g. haemophilia)
CC inhibition of tumour cell proliferation, suppression of an inflammatory
CC response or treatment of a nervous system disorder such as Alzheimer's
CC disease. Detection of the presence or increased expression of the
CC polynucleotide or the protein it encodes is useful for the diagnosis
CC and/or prognosis of one or more types of cancer. The polynucleotide and
CC polypeptide can be used as nutritional sources or supplements and in the
CC screening of chemical compounds as potential drugs
XX
SQ Sequence 1796 BP; 449 A; 420 C; 490 G; 390 T; 0 U; 47 Other;
Query Match 42.6%; Score 679.8; DB 5; Length 1796;
Best Local Similarity 81.6%; Pred. No. 1.2e-170;
Matches 850; Conservative 0; Mismatches 184; Indels 8; Gaps 8;
Qy 295 CAATATGGATTATAAATCTAGCCTGATTCC-TGATGGAAACGCTATGGAGAACCTGGAGA 353
Db 146 CAGAACGGACTATAGTCGAGCCTGACTCCAGGATGGGAATCCCATGGAGAACTGGAGA 205
Qy 354 AGCAGCTGATTCGCCCATCTGCTGGAGGA-TGTTTACCAAGCCTGTGGTCTATCTGCCCC 412
Db 206 TGCAGCTGATCTGGCCTATCTGCCCGAGATTGTGTACCAAGCCGCTGTCTATCTCTGCCG 265
Qy 413 TGCCAAACACACCTCTGCGGGAAGTGC-CAACACACATCTTCCAGGCTGCCAATCCCTTA 471
Db 266 TGCCAGCACACCTCTGCGGGAAGTGTGTCTCAATGACATCTTCCAGGCTGCAAAATCCCTTA 325
Qy 472 CTGGACCAACCGCGGTGGCTCAGTGTCCATGTCTGGAGGTGCTTTCCGTTGCCCTCTGCG 531
Db 326 CTGGACCAACCGCGGCGAGCTCAGTGTCCATGTCTCTGGAGGTGCTTTCCGTTGCCCACTG 385
Qy 532 CGCCCATGAGTGTATGTGACCGGACGCGCAGCGGGTGTA-CGGCTCGAGAGGAAC-TCCTG 589
Db 386 CGCCACGAGGTGTATGTGATCGTACCGGAGTGTACCGTGTGTGACACAGGAACCTTGTG 445
Qy 590 GTGGAAACATCATTTGACATCTTACAAAGCAGGAGTGC-TCCAGTCCGCGCCCTCAGAAAGG 648
Db 446 GTGGAGAACATCATCGACATCTTACAAAGGAGTGTCTTCCAGTCCGCGCCCTCGAAGGC 505

Qy	649	CA-GCCACCCGATGTGCAAGGAAACA	CGAAGACGAGAAAGATCAACATCTACTGHTCTCACGT	707
Db	506	CACGACAACCCATGTGCAAGGAGCACA	GAAAGATGAGAAATCAACATCTACTGTCTCACGT	565
Qy	708	GTGAGGTGCCCTACTTGTCTCTTGTG	CAAGTGTTTGGGGCTCAACAGGCGCTGTCAGGTTG	767
Db	566	GTGAGGTGCCCACTGCTCTCATGTG	CGAGGTGTTTGGGATCCAAGGCGCTGGGAGTGG	625
Qy	768	CCCTTTGGCAAAGCATCTTCCAAGGA	CAGAAGACTGAGCTGAGTAACTGCATCTCCATGC	827
Db	626	CCCAITTCGAGTGTCTTCCAGGGA	CAAAAGACTGAACTGAATCTGTATCTCCATGC	685
Qy	828	TGTTGGCGGGGAACGA	CCGAGTGCGAGACGATCATCTCTCAAGCTGAGAGGA	887
Db	686	TGTTGGCGGGGAATGACCGTGTG	CAGACCATCATCACTCACTGCTGGAGGA	745
Qy	888	TGACCAAGGAGAATAGCCACCAGTGA	A-GGAGGAGCTGAGTCAGAGTTTGCACCCCTC	946
Db	746	TGACCAAGGAGAACAGTCA	CAACGTAATAGAGAGCTGAGCCAGAAGTTTGACACGTTG	805
Qy	947	TACGCCATCTCGATGATAAGAAAG	AGCGAGCTGTGTCAGCGGATCAACGAGGAGCAGGAG	1006
Db	806	TATGCCATCTGGATGAAAAGAAAG	TGAGTTGCTGTCGGATCTCGCAAGAGCAGGAA	865
Qy	1007	GAGAGCTGGGCTTCATCGAGGCTCT	GATCTCTCCAGTACAGGAGGAGAGCTGGAAAAGTCC	1066
Db	866	AAGAAGCTTATCTTCTATCGAGG	CGCCTCATCCAGCAGTACCAGGAGCAGCTGGCAAGTCC	925
Qy	1067	ACCAAGCTTGTGGAGACGGCCAT	CCAGTCTCCTGGATGAGCCGCGAGGGGCTACCTTCCTC	1126
Db	926	ACAAGCTGTGGAACTGCAATCC	AGTCCCTGGAAGAGCTGGGGAGGCACTTTCTC	985
Qy	1127	TCAAGTGCCCAAGCAGCTCAT	CAAGAGCAITGTAGAAGCCTCCAAGGCTGCCAGCTGGGG	1186
Db	986	TTGACTGCCAAGCAACTCAT	CAAAAGCATTTGTGGAAGCTTCCAAGGCGCTGCCAGCTGGG	1045
Qy	1187	AAGACAGACAAAGCTTTGGAACAT	GGCATCTACTCTGACCTTTAGAACACATAGCA	1246
Db	1046	AAGA CAGACAGGGCTTTGAGAAC	ATGGAATCTTTACTTTTGAATTTAGAGCACAATAGCA	1105
Qy	1247	GAGGCCTTGAGGGCAATTGACTTT	TGGGACAGGCTAAAGGATGTGATGTTACATGTTTGACC	1306
Db	1106	GA CGCCCTTGAGGCCATTGACTTT	TGGGACAGATNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1165
Qy	1307	TTTGAAGGCGGCTTCCTCTT	1328	
Db	1166	NNNNNNNNNNNNNNNNNNNNNN	1187	

RESULT 13	AAH90117	AAH90117 standard; cdNA; 1183 BP.	SEQ ID NO: 474.
ID	AAH90117		
XX	AAH90117		
AC	AAH90117;		
XX			
DT	01-OCT-2001 (first entry)		
XX			
DE	Human bone marrow cdNA, SEQ ID NO: 474.		
XX			
KW	Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;		
KW	antiviral; antibacterial; antifungal; anti-HIV; haemostatic;		
KW	immunosuppressive; gene therapy; cytokine cell proliferation;		
KW	cell differentiation modulator; immune disorder; infection; cancer;		
KW	human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200153453-A2.		
XX			
PD	26-JUL-2001.		
XX			
PF	23-DEC-2000; 2000WO-US034960.		

QY 682 GAAGATCAACTACTACTGTCTCACGTGTGAGTGGCTACTTCTCTCTTGTGTGCAAGGTGTT 741
DB |||||
540 GAAATCAACTACTACTGTCTCACGTGTGAGTGGCTACTTCTCTCTTGTGTGCAAGGTGTT 599
QY 742 TGGGGCTCACAGGCTGTGAGTGTGCCCCCTTGCAGAGCATCTTCCAAGGACAGAC 801
DB |||||
600 TGGGATCCACAAGGCTGCGAGGTGGCCCCATTGAGAGTGTCTTCCAAGGACAAAAAGAC 659
QY 802 TGAGCTGAGTAAGTACTGATCTCCATGTGTGTGCGGGGAAACGACGAGTGCAGACATCAT 861
DB |||||
660 TGAATGATATACTGTATCTCATCTGTGTGTGCGGGGATGACCGTGTGACACCATCAT 719
QY 862 CTCTCAGCTGGAGGACTGTGTGAGAGTACCAAGAGAGATAGCCACCAAGGTGAAGGAGA 921
DB |||||
720 CACTCAGCTGGAGGATTCCTGCGAGTGACCAAGAGAGACAGTCCACAGGTAAGGAGA 779
QY 922 GCTGAGTCAGAGTTTGACACCTCTACGCCATCTGGATGAGAGAGAGCGAGTCTCT 981
DB |||||
780 GCTGAGCCAGAAAGTTTGACACCTGTGTATGCCATCTTGGATGAGAGAAAGTGTGCT 839
QY 982 GCAGCGGATCACGAGGACGAGGAGAGAGCTGGGCTTTCATCGAGGCTCTGATCTCCA 1041
DB |||||
840 GCAGCGGATCACGAGGACGAGGAGAGAGCTGGGCTTTCATCGAGGCTCTGATCTCCA 899
QY 1042 GTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCATCCAGTCCCTGGA 1101
DB |||||
900 GTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGAACTGCCATCCAGTCCCTGGA 959
QY 1102 TGAGCCCGGAGGGCTACCTTCTCT 1127
DB |||||
960 CGAGCTGGGGAGCCACCTTCTCT 985

RESULT 14

ABQ79510
ID ABQ79510 standard; DNA; 630 BP.
XX
AC ABQ79510;
XX
DT 05-NOV-2002 (first entry)
XX
DE Rat MURF1 VRV splice form encoding DNA.
XX
KW Muscle atrophy protein; MURF1; MURF3; MAFBX; atrophy; neuroprotective;
KW gene therapy; transgenic; gene; rat; ds.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..630
FT /*tag= a
FT /product= "MURF1 VRV splice form"
FT /partial
FT /note= "the start and stop codons are not indicated"
XX
PN WO200261046-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002811.
XX
PR 30-JAN-2001; 2001US-0264926P.
PR 10-AUG-2001; 2001US-0311697P.
PR 22-OCT-2001; 2001US-0338742P.
XX
XX (REG-) REGENERON PHARM INC.
PA Glass DJ, Bodine SC;
XX
PI WPI: 2002-608513/65.
DR P-PSDB; ABB81142.
XX
PT Isolated nucleic acid molecules encoding muscle atrophy proteins, e.g.

PT MURF1, MURF3 or MAFBX, useful for treating muscle atrophy and other
PT related disorders, e.g. Guillain-Barre syndrome, peripheral neuropathy,
PT and nerve damage.
XX
PS Claim 3; Fig 16; 104pp; English.
XX
CC The invention relates to isolated nucleic acid molecules encoding muscle
CC atrophy proteins MURF1, MURF3, or MAFBX. The proteins can be expressed by
CC standard recombinant methodology. The nucleic acid molecules and
CC polypeptides are useful for treating muscle atrophy or detecting atrophy,
CC and for treating related diseases/disorders, e.g. Guillain-Barre
CC syndrome, peripheral neuropathy, or nerve damage caused by environmental
CC toxins or drugs. The MURF1, MURF3 and MAFBX antagonists, and the
CC antagonists of their pathways are useful for inhibiting atrophy, inducing
CC hypertrichosis, decreasing ubiquitination, interfering with the ubiquitin
CC pathway, or modulating MURF1, MURF3 or MAFBX expression or activity. The
CC nucleotide sequences are useful for diagnostic and genetic testing. The
CC present sequence represents a rat MURF1 VRV splice form encoding DNA
XX
SQ Sequence 630 BP; 153 A; 175 C; 173 G; 129 T; 0 U; 0 Other;

Query Match 34.3%; Score 547.4; DB 6; Length 630;
Best Local Similarity 94.0%; Pred. No. 1.7e-135;
Matches 569; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 295 CAATATGATTAATAAATCTAGCTGATTCCTGATGGAACGCTATGGAGAACCTGGAGAA 354
DB |||||
21 CGACAAGATTATAAATCTGCTTGGATTCGCGACGGAATGCTATGGAGAACCTGGAGAA 80
QY 355 GCAGCTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCTGTGTCATCTGCCCCG 414
DB |||||
81 GCAGCTCATCTGCCCATCTGCTTGGATGTTTACCAAGCTGTGTCATCTGCCCCG 140
QY 415 CCAACACAACTCTGCGGAAAGTGTGCCAACACATCTTCCAGGCTGCGAAATCCCTACTG 474
DB |||||
141 CCAGCAAACTCTGCCGGAAGTGTGCCAACACATCTTCCAGGCTGCCAATCCCTACTG 200
QY 475 GACCAACCGCGTGGCTCAGTGTCCATGTCTGGAGTGGTTCCTGTCGCCCTCGTCCG 534
DB |||||
201 GACCAACCGCGTGGCTCGGTGTCCATGTCTGGAGTGGTTCCTGTCGCCCTCGTCCG 260
QY 535 CCATGAAGTATCATGGACCGGCACGGGTGTACGGCTGCGAGAGAACCTGCTGGTGA 594
DB |||||
261 CCATGAAGTATCATGGACCGGCATGGGTGTACGGTCTGCGAGAGAACCTGCTGGTGA 320
QY 595 AAACATCATTTGACATCTACAAGCAGAGTGTCTCCAGTGGCCCTGCGAGAGGCGAGCCA 654
DB |||||
321 GAACATCATCGACATCTACAAGCAGAGTGTCTCCAGTGGCCCTGCGAGAGGCGAGCCA 380
QY 655 CCCGATGTGCAAGGAACACGAGAGCAGAGAATCAACATCTACTGTCTCACGTGTGAGGT 714
DB |||||
381 CCCGATGTGCAAGGAACACGAGAGCAGAGAATCAACATCTACTGTCTCACGTGTGAGGT 440
QY 715 GCCTACTTGTCTCTTGTGCAAGGTGTGCGGCTGTCAGAGGCTGTGAGGTGCGCCCTTT 774
DB |||||
441 GCCTACTTGTCTCTTGTGCAAGGTGTGCGGCTGTCAGAGGCTGTGAGGTGCGCCCTTT 500
QY 775 GCAAGATCTTCCAAGGACAGAGACTGAGTGAAGTAACTGTCATCTCCATCTGCTGGC 834
DB |||||
501 ACAAAGCATCTTCCAAGGACAGAGACTGAGTGAAGTAACTGTCATCTCCATCTGCTGGC 560
QY 835 GGGGAACGACCGAGTGCAGAGCATCATCTCTCAGCTGGAGGACTGCTGTCAGAGTGAACCA 894
DB |||||
561 AGGGAACGACCGAGTGCAGAGCATCATCTCTCGCAGCTGGAGGACTCTCTGCCGAGTGAACCA 620
QY 895 GGAGA 899
DB |||||
621 GGTGA 625

RESULT 15

ABA99061
ID ABA99061 standard; DNA; 1431 BP.

XX Homo sapiens.
OS WO2003029271-A2.
PN 10-APR-2003.
XX 24-SEP-2002; 2002WO-US030474.
XX 24-SEP-2001; 2001US-0324631P.
XX (HYSE-) HYSEQ INC.
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX WPI; 2003-371981/35.
DR P-PSDB; ADC31154.
XX New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX Claim 1; SEQ ID NO 265; 1185pp; English.
XX The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30899) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1405 BP; 353 A; 360 C; 462 G; 230 T; 0 U; 0 Other;
Query Match 30.2%; Score 481.8; DB 10; Length 1405;
Best Local Similarity 69.4%; Pred. No. 7.7e-118;
Matches 670; Conservative 0; Mismatches 292; Indels 3; Gaps 1;
QY 317 CTGATTCTCTGATGGAAACCTATGGAGAACCTGGAGAACGCTGATCTGCCCATCTGCG 376
DB |||||
313 CTGCTAGGGGATGCACACAGCATGGACACCTGGAGAACGCTCATCTGCCCATCTGCG 372
QY 377 CTGGAGATGTTTACCAAGCTGTGTCATCTCCCTGCCACACACACCTCTGCCGGAAG 436
DB |||||
373 CTGGAGATGTTTCTCCAAACCAAGTGGTGTATCTTGGCCCTGTCACACACACCTGTGCCGCAA 432

QY 437 TGTGCCAAACGACATCTTCCAGGCTGCGAATCCCTACTGGAACCAACCGGGTGGCTCAGTG 496
DB |||||
433 TGTGCCAAACGACGCTTCCAGGCTGCGAATCCCTATATGGCAGTCCCGGGCTCCACCACT 492
QY 497 TCCATGCTCGAGAGTGGTTCGGTTGCCCTCGTGGCCCATGAAGTATCATGAGCCGG 556
DB |||||
493 GTGTCTTCAGGAGCCGTTTCCGCTGCCCATCGTGGCAGGCTAGGTTGTCTCGACACAG 552
QY 557 CACGGGTTGTACCGGCTCGAGAGAACTGTGTTGGTGAAGAACATCATTTGACATCTACAG 616
DB |||||
553 CACGGTGTCTACGGCTCGAGGAACTGTGTTGGTGAAGAACATCATTTGACATTTACAG 612
QY 617 CAGGAGTCTCCAG--TCGGCCCTCGAGAAAGCAGCCACCCCATGTGCGAAGAAACAC 673
DB |||||
613 CAGGAGTCTATCCAGGCTGCTGCTCCAGAGCTGAGCAGCAGCTCATGTGCGAGGAGCAT 672
QY 674 GAAGCAGAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCTTACTTGTCTCTTGGC 733
DB |||||
673 GAAGCAGAGAGATCAATATTTACTGTCTGAGTGTGAGGTGCTTACTTGTCTCTTGGC 732
QY 734 AAGGTGTTTGGGCTCAGCAGGCTGTGAGTGTGCTTGTGCAAGAGCATCTTCAAGAGA 793
DB |||||
733 AAGGTCTTGGTGGCCCAAGGACTGTGAGTGTGCTTGTGCAAGAGCATCTTCAAGAGC 792
QY 794 CAGAACTGAGTGAATCACTTCTCATGTGTTGGTGGGGAAGAACCGAGTGCAG 853
DB |||||
793 CAGAACTGAGTGAATCACTTCTCATGTGTTGGTGGGGAAGAACCGAGTGCAG 852
QY 854 AGCATCATCTCAGCTGAGGACTGTGAGTGTGCTTGTGCAAGAGCATCTTCAAGAGC 913
DB |||||
853 GCAGTGAATCACAAGATGGAGGAGTGTGCTGAGTGTGCTTGTGCAAGAGCATCTTCAAGAGC 912
QY 914 AAGGAGGAGTGTGAGTGAATCACTTCTCATGTGTTGGTGGGGAAGAACCGAGTGCAG 973
DB |||||
913 AAGCAGTGTGTTAACCAGAGTGTGAGTGTGCTTGTGCAAGAGCATCTTCAAGAGC 972
QY 974 GAGTGTGCTGAGCAGGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1033
DB |||||
973 GAGTGTGCTGAGCAGGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1032
QY 1034 ATCTCTCAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1093
DB |||||
1033 ATCTCTCAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1092
QY 1094 TCCCTGAGTGTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1153
DB |||||
1093 TCCATGGAAGAGCCACAATGGCGCTGTATCTCAGCAGGAGGAGGAGGAGGAGGAGGAGG 1152
QY 1154 ATTGTAGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1213
DB |||||
1153 GTCCGGGCGCATGTGCAAGGTTGGAGCTGGCAGGGCGCGGAGCCAGGCTATGAGAGCATG 1212
QY 1214 GACTACTTACTCTGGACTTAGAACACATAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1273
DB |||||
1213 GAGCAATTTACCGTAAAGGTTGGAGCAGCTGGCGGCAATGCTGCGGAGCCATCGACTTCCAG 1272
QY 1274 ACAGG 1278
DB |||||
1273 CCAGG 1277

RESULT 17
AAH68563
ID AAH68563 standard; cDNA; 1913 BP.
XX
AC AAH68563;
XX
DT 13-SEP-2001 (first entry)
XX
DE Human protein HP01115 coding sequence.
XX
KW Human; gene therapy; tumour; ss.

XX Bednarik D, Greene J, White M;
 PI WPI; 2001-570621/64.
 DR P-PSDB; AAG63832.
 XX Nucleic acid encoding a cardiomyopathy associated protein that is
 PT differentially expressed in human left ventricle assist device (LVAD)
 PT myocardial biopsy samples, useful for diagnosing, preventing or treating
 PT cardiomyopathy.
 XX Claim 2; Page 49-51; 55pp; English.
 XX The present sequence encodes a human cardiomyopathy associated protein
 CC (CAP) that is differentially expressed in human left ventricle assist
 CC device (LVAD) myocardial biopsy samples. The predicted isoelectric point
 CC of CAP is approximately 12.2. The CAP polynucleotide and polypeptide are
 CC useful for diagnosing, preventing or treating cardiomyopathy. The
 CC treatment diminishes the occurrence of at least one of the following
 CC symptoms associated with cardiomyopathy: reduced ejection fraction,
 CC increased left ventricular diastolic dimension, decreased ventricular
 CC wall thickness, increased atrial size, valvular regurgitation, exertional
 CC intolerance or ventricular tachyarrhythmia. Modulators of CAP are also
 CC useful for preventing or treating cardiomyopathy
 XX
 SQ Sequence 1990 BP; 524 A; 535 C; 613 G; 318 T; 0 U; 0 Other;
 Query Match 30.2%; Score 481.8; DB 4; Length 1990;
 Best Local Similarity 69.4%; Pred. No. 96-118;
 Matches 670; Conservative 0; Mismatches 292; Indels 3; Gaps 1;
 QY 317 CTGATTCCTGATGAAACGCTATGGAGAACCTGGAGAGCAGCTGATCGCCCATCTGC 376
 Db 310 CTGCTAGGGGATGACACAGCATGACCAACCTGGAGAGCAGCTCATCTGCCCATCTGC 369
 QY 377 CTGGAGATGTTTACCAAGCTGTGTCTATCTCCCTGCGCAACACAACTCTGCCGGAAG 436
 Db 370 CTGGAGATGTTTCTCAAAACCAAGTGTGTCTCCCTGCGCAACACAACTCTGCCGGAAG 429
 QY 437 TGTGCAACGACATCTTCAGGCTCGAATCCTACTTGACCAACCGGGTGGCTCACTG 496
 Db 430 TGTGCAACGACATCTTCAGGCTCGAATCCTACTTGACCAACCGGGTGGCTCACTG 489
 QY 497 TCCATGTCTGGAGTGTGTTTCCGCTGCTCCCTGCGCAACGAGTATGATGACACCGG 556
 Db 490 GTGTCTTCAGGAGGCGGTTTCCGCTGCTCCCTGCGCAACGAGTATGATGACACCGG 549
 QY 557 CACGGGTTGACGGCTGACAGAGAACTCTGTTGGTGGAAACATCATTTGACATCTACAG 616
 Db 550 CACGGTGTCTACGGCTGACAGAGAACTCTGTTGGTGGAAACATCATTTGACATCTACAG 609
 QY 617 CAGGAGTGTCTCAG--TCGGCCCTGCGAAGGCGACCCCGATGTGCAAGGAACAC 673
 Db 610 CAGGAGTGTCTCAGGCGCTGACCTCAAGGCTGAGCAGCCTCATGTGCGAGGAGCAT 669
 QY 674 GAAGACGAGAGATCAACATCTACTGTCTCAGTGTGAGGCTGCTACTTGTCTCTTGTGC 733
 Db 670 GAAGACGAGAGATCAATATTTACTGTCTGAGTGTGAGGCTGCTACTTGTCTCTCTGC 729
 QY 734 AAGGTGTTGGGGCTCACCAGGCTGTGAGTGTGCGCTTTTTCGCAAGCATCTTCCAAAGA 793
 Db 730 AAGGTCTTGGTGTCCCAAGGACTGTGAGTGTGCGCTTTCGCAAGCATCTTCCAAAGA 789
 QY 794 CAGAAGACTGAGCTCAGTAACATCTCTCAGTGTGAGGCTGCGGGAACGACCGAGTGCAG 853
 Db 790 CAGAAGACTGAGCTCAGGATGCGATCTGCTGAGTGTGCGGGAACGACCGAGTGCAG 849
 QY 854 ACATCATCTCTCAGCTGAGGACTCTGTCAGAGTGCAGGAGTGCAGGAGATAGCCACAGGTG 913
 Db 850 GCAGTGTACACAGATGAGGAGGTGTGCGCAGACTATCGAGACATATAGCGGAGGAGCAG 909
 QY 914 AAGGAGGAGTGTGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGG 973

Db 910 AAGCAGTTGTTAAACACGAGGTTTGGAGAGCCTGTGCGCAGTGTGGAGAGCGCAAGGCT 969
 QY 974 GAGCTGTGTCAGCGGATCACGACGAGCAGGAGGAGGAGGAGTGTGCGGCTTTCATCGAGGCTCTG 1033
 Db 970 GAGCTGTGTCAGCGGCTGCGCCGCGGAGCAAGAGGAGAGTGTGCGGCTTTCATCGAGGCTCTG 1029
 QY 1034 ATCTCTCAGTTCAGGAGCAGCTGGAAGAGTCCCAAGCTTGTGGAGAGCAGCCCATCCAG 1093
 Db 1030 ATCTCTCAGTTCAGGAGCAGCTGGAAGAGTCCCAAGCTTGTGGAGAGTGTGCGGCTTTCATCGAGGCTCTG 1089
 QY 1094 TCCCTGTGATGAGCGCGGAGGAGTGTGCTCTCAAGTGTGCAAGCAGCTCATCAAGAGC 1153
 Db 1090 TCCATGGAAGAGCCCAATGCGCTGTATCTCCAGAGGCGCAAGAGTGTGATCAATAG 1149
 QY 1154 ATTGTAGAAGCTCTCAAGGCTGTGCGAGTGTGCGGAGAGCAGAGCAAGGCTTGTGAGAACATG 1213
 Db 1150 GTGCGGCGCATGTGCAAGTGTGAGTGTGCGGAGGCGCGGAGGCTATGAGAGCATG 1209
 QY 1214 GACTACTTCTCTGAGCTTGAACACATAGCAGAGGCTTGTGAGGCGCATGACTTTGGG 1273
 Db 1210 GAGCAATTCACCGTAAGGCTGAGCAGCTGCGGCAATGCTGCGGAGCAGTATGACTTCCAG 1269
 QY 1274 ACAGG 1278
 Db 1270 CCAGG 1274
 RESULT 19
 AAA72433
 ID AAA72433 standard; cDNA; 1349 BP.
 XX AC AAA72433;
 XX DT 19-DEC-2000 (first entry)
 XX XX Human nucleic acid-binding protein NuABP-52 cDNA.
 DE Human nucleic acid-binding protein; NuABP; agonist; antagonist; EST;
 KW expressed sequence tag; drug screening; recombinant expression; antibody;
 KW reproductive disorder; infertility; immunological disorder;
 KW neurological disorder; cell proliferative disorder; cancer; tumour; ss.
 XX Homo sapiens.
 OS WO200044900-A2.
 PN 03-AUG-2000.
 PD 28-JAN-2000; 2000WO-US002237.
 PF 29-JAN-1999; 99US-0117904P.
 PR 29-JAN-1999; 99US-0117905P.
 XX (INCY-) INCYTE PHARM INC.
 PA Tang YT, Lal P, Hillman JL, Yue H, Azimzai Y, Lu AMD, Baughn MR;
 PI Tran B, Shih LL, Au-Young JL;
 XX WPI; 2000-499332/44.
 DR P-PSDB; AAB21048.
 XX Novel nucleic acid binding proteins, used to identify agonists and
 PT antagonists of them, for the treatment of reproductive, immunological,
 PT neurological and cell proliferative disorders including cancer.
 XX Claim 4; Page 178-179; 180pp; English.
 XX Sequences AAA72382-A72436 represent cDNAs encoding novel human nucleic
 CC acid-binding proteins (NuABPs; AAB20997-B21051). These cDNAs were
 CC produced by extension from an appropriate EST (expressed sequence tag)
 CC using primers designed using the EST. The invention also relates to
 CC expression constructs, host cells and transgenic organisms comprising a
 CC human NuABP nucleic acid, recombinant production of the human NuABPs, and

Sequence 867 BP; 204 A; 242 C; 258 G; 163 T; 0 U; 0 Other;

Best Local Similarity 71.5%; Pred. No. 6e-108;

377 CTGGGCA TCTTTTACCA AGCCTCTGCTCATCTCTGCCCTT

db 88 CTGGAGATGTTCTCCAAACCAGTGGTGATCCTGCCCT

QY 437 TGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACT

Db 148 TGTGCCACGACGTCTTCCAGGCTCGAATCCTCTAT

497 TCCATGCTGGAGGTGGTTCCGTTGCCCTCGTGCC

DB Z08 GGTCTTCAGGAGGCCGTTCCTCCCTGCCATCTGTCGA

12

.....

4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
8

289

734 AAGGTGTTTGGGGCTCA CAGGCCCTGTGAGGTTGCCC

db 448 AAGGTCCTTCGGTGCCCAAGGACTGTGAGGTGGCCC

QY 794 CAGAAGACTGAGCTGAGTAACTGCATCTCCATGCTGG

D_b 508 CAGAAGAGTGAGCTCAGCGATGGCATCGCGATGCTGG

854 ACGATCATCTCTCAGCTGGAGGACTCGTGACAGTGA

568 GCAGTGAATCACACAGATGGAGGAGGTGTGCCAGACAT

11

.....

䷗

THE

748 ATCCCTCAGTATGCGCACCGACCTGCACCACTG

1094 TCCCTGGATGACCCGGAGGGGCTACCTTCTCTCTCA

Db 808 TCCATGGAAGAGCCACAAATGGCGCTGTATCTCCAGC

Job time : 846 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2005, 08:37:10 ; Search time 4801 Seconds
(without alignments)
12661.662 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 1597

Sequence: 1 ctcgagattacccttacag.....gaaataaattatctctgtgcc 1597

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611.2	38.3	807	CK603034	AGENCY
2	576.8	36.1	769	CO560583	AGENCY
3	563	35.3	912	BI758535	603022861
4	554.6	34.7	655	CA333888	NISC_1803
5	546.2	34.2	868	BG764060	602737069
6	539.6	33.8	1105	BI754358	603026906
7	538.6	33.7	793	BI754358	603026906
8	519	32.5	721	BI754358	603026906
9	505.6	31.7	1142	BU470941	603363447
10	497.8	31.2	952	BU441018	603323733
11	496.6	31.1	682	BG769996	602745109
12	496.2	31.1	966	BU135007	603119195
13	481.8	30.2	1077	AY411684	Homo sapi
14	478.4	30.0	991	AY411685	Pan trogl
15	477.8	29.9	890	BU107891	603111441
16	474.4	29.7	1083	AY411686	Mus muscu
17	472.8	29.6	803	CK128385	AGENCY
18	460.2	28.8	835	BU438107	603209639
19	457.4	28.6	464	AI644642	vw79b06.x
20	441	27.6	731	CN037969	nm 25 bi7
21	421	26.4	996	BU385902	603583640
22	412.2	25.8	801	BU452003	603216327
23	411.6	25.8	465	BB857510	BB857510
24	411.2	25.7	633	CR767305	DKF2p468L

25	394.4	24.7	800	5	BU220426	603756441
26	389.4	24.4	497	5	EX283938	EX283938
27	381.6	23.9	490	2	AW296154	UI-H-B12-
28	379.2	23.7	1455	3	CR677834	Tetraodon
29	373.2	23.4	1466	3	CR670382	Tetraodon
30	363.4	22.8	387	1	AA838940	vw79b06.x
31	361.8	22.7	852	5	BU382730	603583583
32	359.6	22.5	561	5	BP259752	BP259752
33	359.2	22.5	775	7	CF290486	AGENCY
34	358.4	22.4	786	7	CF289491	AGENCY
35	357.4	22.4	554	5	BP259119	BP259119
36	355	22.2	530	6	CD215266	pgm2n.pk0
37	344.8	21.6	795	2	BE894237	BE894237
38	344.4	21.6	803	7	CK600679	AGENCY
39	342.4	21.4	396	2	BB662281	BB662281
40	342.4	21.4	1155	3	AK052911	Mus muscu
41	341.8	21.4	543	5	BX500821	DKF2p779G
42	340	21.3	927	5	BU129677	603118735
43	335	21.0	699	5	BU385958	60358544
44	333.4	20.9	449	6	CB742808	AMGNNUC.N
45	329.8	20.7	822	5	EX427830	EX427830

ALIGNMENTS

RESULT 1
CK603034
LOCUS
DEFINITION
AGENCY 17899884 NIH_MGC_234 Rattus norvegicus cDNA clone
IMAGE:7193197 5', mRNA sequence.
CK603034
ACCESSION
CK603034
VERSION
CK603034.1
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 807)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM15055 row: b column: 11
High quality sequence stop: 643.
FEATURES
Location/Qualifiers
1..807
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7193197"
/tissue_type="heart, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_234"
/note="Organ: heart; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from pooled heart tissue from a
mix of male and female animals at 8 wk old. Tissues were
snap-frozen and kept at -80C for two days before RNA
extraction and purification (Tri-reagent method). CDNA was
primed using oligo-dr primer:
5'-pGACTAGTTAGATCGGAGCGGCCCC(T)25-3' and cloned into

the EcorV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_233) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN	
Query Match	38.3%; Score 611.2; DB 7; Length 807;
Best Local Similarity	92.7%; Pred. No. 1.1e-150;
Matches	674; Conservative 0; Mismatches 49; Indels 4; Gaps 3;
QY	259 TGTGACGCGAGTGGGCAAGACAGTCCGA-TTTCAAAGCAATATGGATTATAAATCTAGCC 317
Db	1 TGTGACGCGAGTGGGCAAGACAGTCCGAGTTTCGAAGCAATATGGATTATAAATCTGGCT 60
QY	318 TGNATTCTGATGGAACCGCTATGGAACTGGAGAGCAGCTGATCTGCCCATCTGCC 377
Db	61 TGNATTCGGACGGAATGCTATGGAACTGGAGAGCAGCTGATCTGCCCATCTGCC 120
QY	378 TGGAGATGTTTACCAAGCCTGTGCTCATCTGCGCTGCCAACAACCTCTGCGGAAAT 437
Db	121 TTGAGATGTTTACCAAGCCTGTGCTCATCTGCGCTGCCAACAACCTCTGCGGAAAT 180
QY	438 GTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGAACCAACCGCGTGGCTCACTG 497
Db	181 GTGCCAACGACATCTTCCAGGCTGCGCAATCCCTACTGGAACCAACCGCGTGGCTG 240
QY	498 CCATGCTCGGAGTCTGTTCCGCTGCGCTGCGCCCATGAGTGCATGAGTGCACCGGC 557
Db	241 CCATGCTCGGAGTCTGTTCCGCTGCGCTGCGCCCATGAGTGCATGAGTGCACCGGC 300
QY	558 ACGGGGTGTACGGCTGCGAGAGAACTGCTGTGTGAAAACATCATTTGACATCTACAAGC 617
Db	301 ATGGGGTGTACGGCTGCGAGAGAACTGCTGTGTGAAAACATCATTCGACATCTACAAGC 360
QY	618 AGAGTGTCTCCAGTCCGGCCCTGCGAAGAGGCGCAACCCGATGTGCAAGGAACACGAAG 677
Db	361 AGGAATGCTCCAGTCCGGCCCTGCGAAGAGGCGCAACCCGATGTGCAAGGAACACGAAG 420
QY	678 ACAGAGATCAACATCTACTGCTCACTGAGTGTGAGTGTGCTTCTCTTGTGCAAGG 737
Db	421 ACAGAAAAATCAACATCTACTGCTCACGTGCGAGTGTGCTTCTCTTGTGCAAGG 480
QY	738 TGTTCGGGCTCACAGGCTGTGAGTGTGCGCTTTGCAAGCATCTTCCAAAGGACAGA 797
Db	481 TGTTCGGGCTCACAGGCTGTGAGTGTGCGCTTTACAGATCTTCCAAAGGACAGA 540
QY	798 AGACTGAGTGTAGTAACTGCACTCTCATGCTGTGCGGGGAAACGACCGAGTGCAGACA 857
Db	541 AGACTGAACTGAGCAATTGCACTCTCATGCTGTGCGGGGAAACGACCGAGTTCAGACTA 600
QY	858 TCATCTCTCAGCTGGAGGACTGCTGAGAGTACCAAGGAGATAGCCACCGAGTGAAGG 917
Db	601 TCATCTCGAGCTGGAGGACTCTGCGAGTGAACCAANGGAAACAGCCACCGAGTGAAGG 660
QY	918 AGGAGCTGAGTCAGAGATTTGACACCTCTACGCCATCTCGGATGAGAGAGAGCGAGC 977
Db	661 AGGAATGAGCCA-CACTTTGAGCCCTCTACGCCATCTGGA--CAGAGAGAGTGAAC 717
QY	978 TGCTGCA 984
Db	718 TGCTGCA 724

RESULT 2
COS60583
LOCUS
DEFINITION
AGENCOURT 28621713 NIH MGC 250 Rattus norvegicus cDNA clone
IMAGE:7383160 5', mRNA sequence.
ACCESSION
COS60583
VERSION
COS60583.1 GI:50373179
KEYWORDS
EST.
Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 769)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabp3-remail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM41546 row: a column: 14
High quality sequence stop: 683.
Location/Qualifiers
1..769
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7383160"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 250"
/note="Organ: thymus; Vector: pExpress-1; Site 1: EcorV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTAGTCTAGATCGCGAGCGCGCC(T)25-3' and cloned into
the EcorV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.9 kb. This is a
primary library (normalized library is NIH_MGC_251) and
was constructed by Open Biosystems. Note: this is a
NIH_MGC library"

FEATURES
source

Query Match 36.1%; Score 576.8; DB 7; Length 769;
Best Local Similarity 94.1%; Pred. No. 1.4e-141;
Matches 610; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
QY 253 ACTTGGTGTGACGAGTGGGCAAGACAGTCCGA-TTTCAAAGCAATATGGATTATAAAT 311
Db 34 ACTCGGTGTGACGCGAGGTGGAAGAGACAGTCCGAGTTTCGAAGCAATATGGATTATAAAT 93
QY 312 CTAGCCTGATTCTGATGGAAAACGCTATGGAGAACTGGAGAGCAGCTGATCTGCCCA 371
Db 94 CTGGCTTGATTCCGACGGAATGCTATGAGAACTGGAGAGCAGCTCATCTGCCCA 153
QY 372 TCTGCTCGAGATGTTTACCAAGCCTGTGCTCATCTCTGCCCTGCCAACAACCTCTGCC 431
Db 154 TCTGCTTGGAGTGTTTACCAAGCCTGTGCTCATCTCTGCCCTGCCAACAACCTCTGCC 213
QY 432 GGAAGTGTGCCAAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGGGTGGCT 491
Db 214 GGAAGTGTGCCAAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGGGTGGCT 273
QY 492 CAGTGTCCATGTCTGAGGTCTGTTCCGTTGCCCTCTGTCGCCCATGAAGTGCATCG 551
Db 274 CGGTGTCCATGTCTGAGGTCTGTTCCGTTGCCCTCTGTCGCCCATGAAGTGCATCG 333
QY 552 ACCGCGACGGGTGTACGCGCTGCGAGGAACTGCTGTGTGAAAACATCATTTGACATCT 611
Db 334 ACCGCGATGGGTGTACGCTCTGAGAGAACTGCTGTGTGAGAAACATCATCGACATCT 393
QY 612 ACAAGCAGGAGTGTCTTCCAGTCCGCCCTCTGCAGAAAGGCGACCCCGATGTGCAAGAAC 671

ORIGIN

Query Match 36.1%; Score 576.8; DB 7; Length 769;
Best Local Similarity 94.1%; Pred. No. 1.4e-141;
Matches 610; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
QY 253 ACTTGGTGTGACGAGTGGGCAAGACAGTCCGA-TTTCAAAGCAATATGGATTATAAAT 311
Db 34 ACTCGGTGTGACGCGAGGTGGAAGAGACAGTCCGAGTTTCGAAGCAATATGGATTATAAAT 93
QY 312 CTAGCCTGATTCTGATGGAAAACGCTATGGAGAACTGGAGAGCAGCTGATCTGCCCA 371
Db 94 CTGGCTTGATTCCGACGGAATGCTATGAGAACTGGAGAGCAGCTCATCTGCCCA 153
QY 372 TCTGCTCGAGATGTTTACCAAGCCTGTGCTCATCTCTGCCCTGCCAACAACCTCTGCC 431
Db 154 TCTGCTTGGAGTGTTTACCAAGCCTGTGCTCATCTCTGCCCTGCCAACAACCTCTGCC 213
QY 432 GGAAGTGTGCCAAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGGGTGGCT 491
Db 214 GGAAGTGTGCCAAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGGGTGGCT 273
QY 492 CAGTGTCCATGTCTGAGGTCTGTTCCGTTGCCCTCTGTCGCCCATGAAGTGCATCG 551
Db 274 CGGTGTCCATGTCTGAGGTCTGTTCCGTTGCCCTCTGTCGCCCATGAAGTGCATCG 333
QY 552 ACCGCGACGGGTGTACGCGCTGCGAGGAACTGCTGTGTGAAAACATCATTTGACATCT 611
Db 334 ACCGCGATGGGTGTACGCTCTGAGAGAACTGCTGTGTGAGAAACATCATCGACATCT 393
QY 612 ACAAGCAGGAGTGTCTTCCAGTCCGCCCTCTGCAGAAAGGCGACCCCGATGTGCAAGAAC 671

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
 Plate: LLAM12387 row: D column: 17
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers
 1. .655
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="IMAGE:5599072"
 /sex="male"
 /tissue type="dorsolateral prostate, pool of 3-, 5-, and 7-days post-castration"
 /dev_stage="adult, 11 week"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Pr50"
 /notes="Organ: prostate; Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV; Cloned unidirectionally. Primer: Oligo dt. Pool of 3 primary libraries: NCI_CGAP_Pr39 (dorsolateral prostate from 11 wk male, 3 days post-castration, average insert size 2.7 kb), NCI_CGAP_Pr29 (dorsolateral prostate from 11 wk male, 5 days post-castration, average insert size 2.2 kb) and NCI_CGAP_Pr42 (dorsolateral prostate from 11 wk male, 7 days post-castration, average insert size 2.2 kb). Constructed by Life Technologies/Invitrogen. Note: this is a NCI_CGAP Library."

FEATURES

source

Query Match 34.7%; Score 554.6; DB 6; Length 655;
 Best Local Similarity 94.4%; Pred. No. 1.1e-135;
 Matches 586; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
 253 ACTTGGTGTGACAGGTGGGCAAGACAGTCGCA-TTTCAAAGCAATATGGATTATAAAT 311
 35 ACTCGGTGTGACGAGGTGGAAGACAGTCGCGAGTTTGGAGCAATATGGATTATAAAT 94
 312 CTAGCCCTGATTCTGTATGGAACGCTATGGAGAACCTTGGAGAGCAGTGTATCTGCCCA 371
 95 CTGGCTTGATTCTGGACGGAATGCTATGGAGAACCTTGGAGAGCAGTGTATCTGCCCA 154
 372 TCTGCTGTGAGATGTTTACCAAGCTGTGTCTATCTGCTGCCCAACCAACCTCTGCC 431
 155 TCTGCTGTGAGATGTTTACCAAGCTGTGTCTATCTGCTGCCCAACCAACCTCTGCC 214
 432 GGAAGTGTGCAACGACATCTTCCAGGCTGCGAATCCCTA CTGGACCAACCGGGTGGCT 491
 215 GGAAGTGTGCAACGACATCTTCCAGGCTGCGAATCCCTA CTGGACCAACCGGGTGGCT 274
 492 CAGTGTCCATGCTGAGAGTGTGTTTCCGCTGCCCTCTGCTGCCCAATGAAGTATCATGG 551
 275 CGGTGTCCATGCTGAGAGTGTGTTTCCGCTGCCCTCTGCTGCCCAATGAAGTATCATGG 334
 552 ACCGGACAGGGGTACGGCTCCAGAGGAACCTGCTGTGGGAAACATCATTTGACATCT 611
 335 ACCGGATGGGGGTACGGCTCCAGAGGAACCTGCTGTGGGAAACATCATTCGACATCT 394
 612 ACAAGCAGGAGTGTCTCCAGTGGGCGCTTGAGAAAGGACGACACCCGATGTGCAAGAAC 671
 395 ACAAGCAGGAGTGTCTCCAGTGGGCGCTTGAGAAAGGACGACACCCGATGTGCAAGAAC 454
 672 ACAAGCAGGAGTGTCTCCAGTGGGCGCTTGAGAAAGGACGACACCCGATGTGCAAGAAC 731
 455 ACAAGCAGGAGTGTCTCCAGTGGGCGCTTGAGAAAGGACGACACCCGATGTGCAAGAAC 514
 732 GCAAGGTGTTTGGGGCTCACAGGCTGTGAGGTGTCCTTTGCAAGAGCATCTTCCAAG 791
 515 GCAAGGTGTTGCGGGCTCACAGGCTGTGAGGTGTCCTTTGCAAGAGCATCTTCCAAG 574
 792 GACAGAAGACTGAGCTGAGTAACTGCATCTCCATGTGCTGTGGCGGGAAACGACCGAGTGC 851

ORIGIN

Query Match 34.2%; Score 546.2; DB 4; Length 868;
 Best Local Similarity 85.0%; Pred. No. 2e-133;
 Matches 669; Conservative 0; Mismatches 113; Indels 5; Gaps 5;
 262 GACGACAGTGGGCAAGACAGTCGCAATTTCAAAGCAATATGGATTATAAATCTAGCTGAT 321
 83 GAGGACAGCTAGCGTGGCTCTCTATTCTTCCACAGATGGATTATAAGTCGAGCCTGAT 142
 322 TCTGTGATGAAACCGTATGGAGAACTCTGGAGAGCAGCTGATCTGCCCTATCTGCCCTGA 381
 143 CCAGGATGGAAATCCCAAGAGAACTTGGAGAGCAGCTGATCTGCCCTATCTGCCCTGA 202
 382 GATGTTTACCAAGCCTGTGTCTCATCTGCTGCCCTGCCCAACCAACCTCTGCCGGAAGTGTGC 441
 203 GATGTTTACCAAGCAGTGTGTCTCATCTTGGCGTGCACACACACCTGTGCCGGAAGTGTGC 262
 442 CAAACGACATCTTCCAGGCTGCGAATCCCTACTGTGGAACCAACCGCGGTGGCTCAGTGTCCAT 501

575 GACAGAAGACTGAACCTAGCAATTTGCATCTCCATGTGCTGGTGAGGAACGACCGAGTTC 634
 852 AGACGATCATCTCTCAGCTGG 872
 635 AGACTATCATCTCGCAGCTGG 655

RESULT 5

LOCUS

BG764060 868 bp mRNA linear EST 15-MAY-2001
 602737069F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4862321 5',
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BG764060.1 GI:14074713
 Homo sapiens (human)
 Homo sapiens
 Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1722 row: j column: 18
 High quality sequence stop: 863.

FEATURES

source

1. .868
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4862321"
 /tissue type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 49"
 /note="Organ: skin; Vector: pOT87; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 34.2%; Score 546.2; DB 4; Length 868;
 Best Local Similarity 85.0%; Pred. No. 2e-133;
 Matches 669; Conservative 0; Mismatches 113; Indels 5; Gaps 5;
 262 GACGACAGTGGGCAAGACAGTCGCAATTTCAAAGCAATATGGATTATAAATCTAGCTGAT 321
 83 GAGGACAGCTAGCGTGGCTCTCTATTCTTCCACAGATGGATTATAAGTCGAGCCTGAT 142
 322 TCTGTGATGAAACCGTATGGAGAACTCTGGAGAGCAGCTGATCTGCCCTATCTGCCCTGA 381
 143 CCAGGATGGAAATCCCAAGAGAACTTGGAGAGCAGCTGATCTGCCCTATCTGCCCTGA 202
 382 GATGTTTACCAAGCCTGTGTCTCATCTGCTGCCCTGCCCAACCAACCTCTGCCGGAAGTGTGC 441
 203 GATGTTTACCAAGCAGTGTGTCTCATCTTGGCGTGCACACACACCTGTGCCGGAAGTGTGC 262
 442 CAAACGACATCTTCCAGGCTGCGAATCCCTACTGTGGAACCAACCGCGGTGGCTCAGTGTCCAT 501

DEFINITION		603363447F1 CSEQRB21 Gallus gallus cDNA clone ChEST258n11 5', mRNA sequence.	
ACCESSION		BU470941	
VERSION		BU470941.1 GI:25964518	
KEYWORDS		EST.	
SOURCE		Gallus gallus (chicken)	
ORGANISM		Gallus gallus	
REFERENCE		1 (bases 1 to 1142) Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J. Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus. Phasianinae; Gallus. 1 (bases 1 to 1142) Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J. A Comprehensive Collection of Chicken cDNAs Curt. Biol. 12 (22), 1965-1969 (2002)	
AUTHORS		Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.	
TITLE		A Comprehensive Collection of Chicken cDNAs	
JOURNAL		Curt. Biol. 12 (22), 1965-1969 (2002)	
MEDLINE		22335534	
PUBMED		12445392	
COMMENT		Contact: Simon Hubbard Department of Biomolecular Sciences University of Manchester Institute of Science and Technology (UMIST) PO Box 88, Manchester, M60 1QD, UK Tel: 01612008930 Fax: 01612360409 Email: Simon.Hubbard@umist.ac.uk.	
FEATURES		Location/Qualifiers 1..1142 /organism="Gallus gallus" /mol_type="mRNA" /strain="Layer" /db_xref="taxon:9031" /clone="ChEST258n11" /sex="Female" /dev_stage="adult" /lab_host="DH10B" /clone_lib="CSEQRB21" /note="Organ: ovary; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."	
ORIGIN		Query Match 31.7%; Score 505.6; DB 5; Length 1142; Best Local Similarity 74.8%; Pred. No. 1.3e-122; Matches 687; Conservative 0; Mismatches 224; Indels 7; Gaps 4; QY 299 ATGGATTATAAATCTAGCCCTGATTCCTGATGAAACCGCTATCGAGAACTCGAGAACTCGAGAAAGCAG 358 Db 60 ATGGATTTCCAGCCCAAGCATCTCGCGATGGCAGCCCATCGAGAGCTCGAGAGAGCAG 119 QY 359 CTGATCTGCCCATCTGCTCGCTGGAGATGTTTACCAAGCCTGTGTGTCATCTCTGCCCTGCCAA 418 Db 120 CTGCTGTGCCCATCTGCTCGCTGGAGATGTTTCAGCAAGCCTGTGTGATCTCTGCCCTGCCAA 179 QY 419 CACAACCTCTGCCGGAAGTGTGCCAAGCATCTTCCAGGCTGCGAATCCCTACTGAC 478 Db 180 CACAACCTCTGCCGGAAGTGTGCCAAGCATCTTCCAGGCTGCGAATCCCTACTGAC 239 QY 479 AACCCGGGGTCTCAGTGTCCATGTCTGGAGGTCTGTTCCGTTTCCCTTGGCCCTCGTCCGCCCAT 538 Db 240 AGCCGAGGAGCAGCAT---CATCTCGGAGCCCGGTTCCGCTGCCCTTACGTGCCGCCAC 296 QY 539 GAAGTGCATGACCGGACCGGGGTGTACGGGCTTCAGAGGAACCTGCTGTGTGGAAC 598 	

RESULT 9
BU470941
LOCUS

Db 297 GAGGTCTGCTGACCGCCACGGTCTATGGGCTGCAGAGGAACCTGCTGGTGGAGAAC 356
Qy 599 ATCAATTGACATCTACAGCAGGAGTCTCCAGTGGCGCCCTGCAGAAAGCAGCACCG 558
Db 357 ATCATCGACATCTACAGCAGGAGTCTCCAGCAGGCCACTCAAGAAAGGGGAGCACCCC 416
Qy 659 ATGTGCAAGGAACACGAAGACGAGAAGATCAACATCTACTGTCTACGCTGTGAGGTGCT 718
Db 417 ATGTGCAAGGAGATGAGACGAGCGATCAACATCTACTGTCTACGCTGTGAGGTGCT 476
Qy 719 ACTTGCTCTTGTGCAAGGTGTTGGGGCTCACAGCCCTGTGAGGTGCTCCCTTTGCAA 778
Db 477 ACTTGCTCTTGTGCAAGGTGTTGGGGCTCACAGCCCTGTGAGGTGCTCCCTTTGCAA 536
Qy 779 AGCATTTCCNAGGACAGAGATGAGTGAATGATCTCCATCTCCATGCTGGTGGCGGG 838
Db 537 AGCATTTCCNAGGACAGAGATGAGTGAATGATCTCCATCTCCATGCTGGTGGCGGG 595
Qy 839 AACGACCGAGTGCAGACGATCATCTCTCAGTGGAGACTCGTGACAGAGTGACCAAGGAG 898
Db 596 AACGACCGAGTGCAGACGATCATCTCTCAGTGGAGACTCGTGACAGAGTGACCAAGGAG 555
Qy 899 AATAGCCACGAGTGAAGGAGGAGTGAATGATGAGTGAATGATGAGTGAATGAGTGAAT 958
Db 656 AACAGCGAGGACGACCAAGCAGGAGTCTGTGCACGTTTGTGATGCGTTCTCAGCGCTG 715
Qy 959 GATGAGNAGNAGCAGCTGCTGCAGCGGATCAGCAGGAGCAGGAGGAGGAGCTGGGC 1018
Db 716 GAGGAGNAGNAGCAGCTGCTGCAGCGGATCAGCAGGAGCAGGAGGAGGAGGAGCAGC 775
Qy 1019 TTCTATCGAGGCTCTGATCTCTCCA--GTACAGGAGCAGCTGGA-AAAGTCCACCAAGCTT 1075
Db 776 TTGTGCGGAGACTCATCACAGATACAGAGGATGAGGAGGATGAGGAGGAGGAGGAG 835
Qy 1076 GTGAGACCGCCATCCAGTCCCTGGATGAGCCCGAGGGGCTACCTTCTCTCAAGTGCC 1135
Db 836 GTGAGACCGCCATCCAGGCGATGAGGAGGAGCGCGCGCGCGCTTCTCTCATGAACGCC 895
Qy 1136 AGCAGCTCATCAAGAGCATTTAGAGGCTTCAAGGCTGCGAGGCTGGGAGGAGCAGAG 1195
Db 896 AGCAGCTCATTAAGAGCATTTAGAGGCTTCAAGGCTGCGAGGCTGGGAGGAGCAGAG 955
Qy 1196 CAAGGCTTTGAGAACATG 1213
Db 956 CAAGGCTATCAGACTTG 973

RESULT 10
LOCUS BU241018 952 bp mRNA linear EST 26-NOV-2002
DEFINITION 603232733F1 CSOQCHN33 Gallus gallus cDNA clone ChEST253a10 5', mRNA sequence.
ACCESSION BU241018
VERSION BU241018.1 GI:25487197
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 952)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
PUBMED
Contact: Simon Hubbard
Department of Bionmolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .952
/organism="Gallus gallus"
/mol_type="mRNA"
/strains="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST253a10"
/sex="Female"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="CSOQCHN33"
/note="Organ: liver; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

Query Match 31.2%; Score 497.8; DB 5; Length 952;
Best Local Similarity 75.5%; Pred. No. 1.4e-120;
Matches 657; Conservative 0; Mismatches 208; Indels 5; Gaps 3;

Qy 426 TCTGCGGAGGTGTCACAGACATCTTCAGGCTGCGAATCCCTACTGGACCAACCGG 485
Db 3 TCTGCGGAGGTGTCACAGACATCTTCAGGCTGCGAATCCCTACTGGAGAGCGAG 62
Qy 486 GTGGTCTAGTCCATGCTGGAGTCTCGTTCCGTTGGCCCTCGTCCGCCATGAAGTGA 545
Db 63 GCAGAGCAT---CATCTCGGAGGCGCGTTCCGTTGCCCTAGTCCGCCACGAGTCC 119
Qy 546 TCATGACCGGACCGGGGTGTACGGCTGCAGAGAACCTGCTGTGGTGGAAACATCATTTG 605
Db 120 TCTGAGCGCCACCGTGTCTATGGCTGCAGAGGAACCTGCTGTGGTGGAGAACATCATCG 179
Qy 606 ACATCTACAGCAGAGTCTCAGTCGCGCCCTGCAGAAAGCAGCACCACCGATGTGCA 665
Db 180 ACATCTACAGCAGAGTCTCAGTCGCGCCCTGCAGAAAGCAGCACCACCGATGTGCA 239
Qy 666 AGGAACAGCAGACGAGAGATCAACATCTACTGTCTCAGTGTGAGGTGCTTACTTGTCT 725
Db 240 AGGAGCATGAGCAGCAGCGGATCAACATCTACTGTCTCAGTGTGAGGTGCTTACTTGTCT 299
Qy 726 CCTTGTGCAAGGTGTTGGGGCTCACCAGGCTGTGAGGTGCGCCCTTTGCAAGCATCT 785
Db 300 CCATGTGCAAGGTCTTCGGTGTCTCACAAGACTGGAGTGGCCCTCTGCGAGAGCATCT 359
Qy 786 TCCAGGACAGAAAGTGTGAGTGAATGATCTCCATGCTGTGCTGGCGGGGAGACACC 845
Db 360 TCCAGGGCCAGAAAGCAGGATTTCAACATTTCCATGCTAGTGGCGGGGAGACACC 419
Qy 846 GAGTGCAGACGATCATCTCTCAGTGTGAGGACTCGTGAGAGTGAGCAAGGAGAAATAGCC 905
Db 420 GCATCCAGACCATCATCTCCAGCTGGAGATTTCTCCGCGAGCACTGAGGAGAACAGCG 479
Qy 906 ACCAGGTGAAGGAGGAGTGTGAGTTCAGAAATTTGACACCTCTACGCCATCTCTGGATGGA 965
Db 480 AGGACGCCAAGCAGGAGCTCTGTGC-ACGTTTGTGTCGTTCTCAGCGTGTCTGGAGGAGA 538
Qy 965 AGAAGGCGAGTGTGTCAGCGGATCAGCAGGAGCAGGAGGAGGAGTGGGCTTTCATCG 1025
Db 539 AGAAGCAGGAGTGTGTCAGCGGATCAGCAGGAGCAGGAGGAGGAGGAGGAGGAGGAG 598

FEATURES
source

QY 1026 AGGCTCTGATCTCCAGTACAGGGAGCAGCTCGAAAAAGTCCACCAAGCTTGTGGAGACCG 1085
 DB 599 AGGGCTCATCCACAAGTACAAAGGAGCAGCTGGAGAAGTCCAGCCGGCTGGTGGAGACGG 658
 QY 1086 CCATCAGTCCCTGATGATGAGCCGAGGGGCTACTCTCTCAAGTGCACAGCAGCTCA 1145
 DB 659 CCATCAGGCCATGAGGAGACCGCGGGCGCGCTTCTCTATGAACCGCCAGCAGCTCA 718
 QY 1146 -TCAAGAGCATTTAGAACCTTCAAGGGCTCCAGCTGGGGAAGACAGAGCAAGGCTTT 1204
 DB 719 TTTAAACGATTTAGAGGCTTCAAGGGCGGCGCTGGAGAAGATTGAGCAAGGCTAT 778
 QY 1205 GAGAACATGAGTACTTACTCTGACCTTGAACACATAGCAGAGCCCTTGAGGCCCAT 1264
 DB 779 GAGAACCTGGATGCTTCAAGTCAAGTCTTGAGCACCTCGCTGATGCGCTCGCGCGCTGG 838
 QY 1265 GACTTTGGACAGGTAAAGGATGATGTT 1294
 DB 839 GACTTTGGACAGGTAAAGGATGATGTT 868

RESULT 11
 BG769996 682 bp mRNA linear EST 15-MAY-2001
 LOCUS 602745109F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4877858 5',
 DEFINITION mRNA sequence.
 ACCESSION BG769996
 VERSION BG769996.1 GI:14080649
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 682)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rc@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1GM1763 row: b column: 03
 High quality sequence stop: 671.
 Location/Qualifiers
 1. .682
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4877858"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 49"
 /notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library. |"

FEATURES

source
 RESULT 12
 BUI35007
 LOCUS 603119195F1 CSEQCHL22 Gallus gallus cDNA clone ChEST78m23 5', mRNA
 DEFINITION sequence.
 ACCESSION BUI35007
 VERSION BUI35007.1 GI:25347936
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 966)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 12445392
 PUBMED
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)

ORIGIN

Query Match 31.1%; Score 496.6; DB 4; Length 682;
 Best Local Similarity 85.7%; Pred. No. 2.7e-120;
 Matches 575; Conservative 0; Mismatches 94; Indels 2; Gaps 2;

QY 630 GTCGGCCCTCGAGAAAGGAGGAGCCAGATGTGCAAGAAACACGACGAGAAGATCA 689
 DB 2 GTCGGCCCTCGAGAAAGGAGGAGTCACTCCCATGTGCAAGAGAGCAAGATGAGAAAATCA 61
 QY 690 ACATCTACTGCTCACTGCTGAGGTGCTTCTTGTCTCTTGTGCAAGGTGTTTGGGGCTC 749
 DB 62 ACATCTACTGCTCACTGCTGAGGTGCTTCTTGTCTCTTGTGCAAGGTGTTTGGGATCC 121
 QY 750 ACCAGGCTGTGAGGTGCTTCTTGTGCAAGCATCTTCCAAGGACAGAAAGCTGAGCTGA 809
 DB 122 ACAAGGCTGTGAGGTGCTTCTTGTGCAAGCATCTTCCAAGGACAGAAAGCTGAGCTGA 181
 QY 810 GTRACTGATCTCCATGCTGTGGGGGAGAGCCAGTGCAGAGCATCTCTCTCAGC 869
 DB 182 ATAACCTGTATCTCCATGCTGTGGGGGAGAGCCAGTGCAGAGCATCTCTCTCAGC 241
 QY 870 TGGAGGACTCTGTGAGAGTGAACCAAGAGAAATAGCCACAGGTGAAGGAGGAGCTGAGTC 929
 DB 242 TGGAGGATCTCGTGTGAGTGAACCAAGAGAAACAGTCAACAGGTAAAGGAGAGCTGAGCC 301
 QY 930 AGAAGTTTGACACCTCTTACGCCATCTCTGGATGAGAAAG- AAGAGCGAGCTGCTGAGCGG 988
 DB 302 AGAAGTTTGACACCTCTTATGCCATCTCTGGATGAGAAAGAAACAGTGTGCTGAGCGG 361
 QY 989 ATCAGCAGGAGCAGGAGAGAGTGGGCTTATCGAGGCTCTGATCTCTCAGTACAGG 1048
 DB 362 ATCAGCAGGAGCAGGAGAGAGTGGGCTTATCGAGGCTCTGATCTCTCAGTACAGG 421
 QY 1049 GAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGAGCGCCATCCAGTCCCTGATGAGGCC 1108
 DB 422 GAGCAGCTGGAAAGTCCACCAAGCTTGTGGAAAGCTGCAATCCATCCCTGAGCAGGCT 481
 QY 1109 GGAGGGCTACCTTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATTTG-TAGAAGCCTTC 1167
 DB 482 GGAGGGCAGCCTCTCTTGTGCTGCCAAGCAACTCATCAAAAGCATTTGCTGGAAGCTCC 541
 QY 1168 CAAGGGCTGCAGCTGGGGAGAGCAGAGCAAGGCTTTGAGAACATGGACTACTTACTCT 1227
 DB 542 CAAGGGCTGGCAGCTGGGGAGAGCAGAGCAGGGCTTTGAGAACATGGACTACTTACTCT 601
 QY 1228 GGACTTAGAACACATAGCAGAGGCTTGGAGGCCATTCAGTCTTGGGACAGGTAAAGGATG 1287
 DB 602 GGATTTAGACACATAGCAGAGCCCTGAGAGCCATTCAGTCTTGGACAGATGAGGAGA 661
 QY 1288 TGATGTTTACAT 1298
 DB 662 GGAAGAATCAT 672

RESULT 12
 BUI35007
 LOCUS 603119195F1 CSEQCHL22 Gallus gallus cDNA clone ChEST78m23 5', mRNA
 DEFINITION sequence.
 ACCESSION BUI35007
 VERSION BUI35007.1 GI:25347936
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 966)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 12445392
 PUBMED
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)

PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

[illegible]

ORIGIN

Query Match	31.1%;	Score 496.2;	DB 5;	Length 966;
Best Local Similarity	74.5%;	Pred. No. 3.9e-120;		
Matches 692;	Conservative 0;	Mismatches 228;	Indels 9;	Gaps 5;
QY	299	ATGGAATTATAAATCTAGCCCTGATTCTCTGATGTGAAACGCTATGGAGAACCTTGGAGAACCTGGAGAAGCAG	358	
DB	39	ATGGATTTCAGCCGCCAGCATCTCGCGGCGATGGCAGCCCATATGGAGGCTTGGAGAACGAG	98	
QY	359	CTGATCTGCCCCATCTGCTCGGAGATGTTTACCAAGCCTGTGTGTCATCTGCGCCCTGCGAA	418	
DB	99	CTGCTGTGCCCCATCTGCTCGGAGATGTTTTCAGCAAGCCTGTGTGTGATCTTCCCTCGCCCTGCGAA	158	
QY	419	CACAACCTCTGCGGAGTGTGCCAAAGCATCTTCCAGAGCTGCGAATCCCTACTCTGACCC	478	
DB	159	CACAACCTCTGCGCAAGTGTGCCAAGCATCTTCCAGGCTGCCAACCCGTACTCTGGAG	218	
QY	479	AACCGGCTGGCTCAGTGTCCATGTCTGGAGGTCTGTTCCGTTGCCCCCTCTGTGCGCCAT	538	
DB	219	AGCCGAGCAGCAGCAT--CATCTCGGAGGCGGTTCCGCTGCCCTACGTGCGCGCAC	275	
QY	539	GAAGTGATCATGACCGGACCGGGTCTACGGCTGCAGAGGACCTGCTGGTGGGAAC	598	
DB	276	GAGGTCTGCTGACCGCCACGGTGTCTATGGGCTGCAGAGAACCTGCTGGTGGGAAC	335	
QY	599	ATCATTTGACATCTACAAGCAGGAGTGTCTCCAGTCTGGGCCCTTGCAAGAAGGCAGCACCCG	658	
DB	336	ATCATCGACATCTACAAGCAGGAGTCTTCCAGCAGGCCCATCAAGAAGGGGAGCACCCC	395	
QY	659	ATGTGCNAGAAACGAAAGACGAGAAGATCAACATCTACTGTCTCAGTGTGAGGTGCTT	718	
DB	396	ATGTGCAAGAGCATGAGGACGAGCGGATCAACATCTACTGCGTCACTGCGAGTGTCCC	455	
QY	719	ACTTGTCTCTTGTGCAAGTGTGTTGGGGCTCACCAAGCCTGTGAGGTGGCCCTTTGCA	778	
DB	456	ACCTGTCTCATGTGCAAGGTCTTCGGTGTCTCAAGAAGACTGCGAAGTGGCCCCCTCTGAG	515	
QY	779	AGCATCTTCCAAGACAGAAAGATGAGCTGAGTAACTGCAATCTCCATGCTGGTGGCGGGG	838	
DB	516	AGCATCTTCCAGGCGCCAGAAAGACGAGTGTAAACAACTGCAATTCATGCTAGTGGCGGGG	575	
QY	839	AACGACCGTGTGACAGCATCTCTCTCAGCTGGAGCATCTGTCGACAGTGAACCAAGGAG	898	
DB	576	AACGACCGCATCAGACCATCATCTCCAGCTGGAGATTCCTGCCGACGACATGTAGGAG	635	
QY	899	AATAGCCACAGGTGAAGGAGGAGCTGAGTCAGAAAGTTTTCACACC--CTTACGCCCATCC	956	
DB	636	AACAGCGAGGACGACCAAGCAGGAGCTCTGTGCAAGTGTGATGTCGTTTCTCAGCGTCTC	695	

Qy	957	TGATGAGAGAGAGACGAGCTCTCGACGGGATACACGACGAGACGAGGAGAAAGCTGG	1016
Db	696	TGGAGGAGAGAGAGACGAGCTCTCTGGACGCATCACCCGCGACGAGGAGCAAGACAA	755
Qy	1017	GCCTTCATCAGGGCTCTGATCTCCAGTACAGGAGAGAGCTGGAAAAAGTCCACCAAGCTTG	1076
Db	756	GCCTTTGTGACGGGCTCATCCCAAGTACAAAGAGACAGCTTGGAGAAAGTCCACGCCGCTTG	815
Qy	1077	TGGAGACCGGCATTCAGATCCCTCGATGAGCCCGAGAGGGGCTACCTT-CTCTCAAGTGCC	1135
Db	816	TGGAGACGGCATCCAGGCCATGAGGAGGAGACCGCGGGGCCCGCTTCCCTCATGAAGGCC	875
Qy	1136	AAGCA--GCTCATCAAGAGCATTTGTAGA-AGCTCCAAGGGCTCCAGCTGGGGGAAGACA	1192
Db	876	AAGCAAGCTCCATTAATAACGATTTGATAGGGCCCTACAAGGGCGGAGGCTTGAAAAAGAT	935
Qy	1193	GAGCAGGGCTTTGAGAACATGGACTACTT	1221
Db	936	TGAGCAAGGTATGAGAACTTTGGATGCGCTT	964
RESULT 13			
LOCUS	AY4111684	1077 bp DNA linear GSS 16-DEC-2003	
DEFINITION	Homo sapiens RNF30 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY4111684		
VERSION	AY4111684.1	GI:39767652	
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1077)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..1077		
gene	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
	<1..>1077		
	/gene="RNF30"		
	/locus_tag="HCM4306"		
ORIGIN			
Query Match	30.2%	Score 481.8; DB 9; Length 1077;	
Best local Similarity	69.4%	Pred. No. 2.7e-116;	
Matches	670; Conservative	0; Mismatches 292; Indels 3; Gaps 1;	
Qy	317	CTGATTCCTCATGGAACGCTATGGAGACCTTGGAGAGCAGCTGATCTGCCCACTGC	376
Db	28	CTGCTAGGGGATGCACACAGCATGGACACCTTGAGAGAGCAGCTCATCTGCCCACTGC	87
Qy	377	CTGGAGATGTTTACCAGCGCTGTGGTCACTCTGCCCTTGCCAAACACAACTCTGCCGAAG	436

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2005, 08:20:04 ; Search time 6747 Seconds
(without alignments)
11469.243 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 1597

Sequence: 1 ctcgagattacccttacag.....gaaataaattatctcgtagc 1597

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1597	100.0	1597	6	AX418852
2	919.4	57.6	1858	10	BC061824 Rattus no
3	917.8	57.5	1861	10	AY059627 Rattus no
4	803.8	50.3	2097	9	AJ291713 Homo sapi
5	802.2	50.2	1756	9	AJ276484 Human mRNA
6	802.2	50.2	1764	6	AX274927 Sequence
7	802.2	50.2	1764	9	BC080529 Homo sapi
8	802.2	50.2	1791	9	AF353673 Homo sapi
9	800.6	50.1	1764	6	AX714538 Sequence
10	800.6	50.1	1764	9	AK056942 Homo sapi
11	799.2	50.0	1041	9	BT007373 Homo sapi
12	799.2	50.0	1041	12	BT008198 Homo sapi
13	747.8	46.8	1757	6	AR220796 Sequence
14	747.8	46.8	2110	6	AX576231 Sequence
15	613.6	38.4	1248	5	BX929474 Gallus ga
16	612	38.3	1277	5	BX931246 Gallus ga
17	489.8	30.7	1450	10	BC083706 Rattus no
18	484.6	30.3	1431	6	AX418848 Sequence
19	484.6	30.3	1448	10	AF294790 Mus muscu

20	482.4	30.2	1270	5	BX934363
21	481.8	30.2	1077	6	CQ721328
22	481.8	30.2	1913	6	E63706
23	481.8	30.2	1913	6	BD095383 Human pro
24	476.8	29.9	1557	5	BC072166 Xenopus 1
25	432.2	27.1	2590	6	AX418850 Sequence
26	431.8	27.0	1865	5	BC077305 Xenopus 1
27	430.6	27.0	1741	9	BC007750 Homo sapi
28	430.6	27.0	1925	6	AX747148 Sequence
29	430.6	27.0	1925	9	AK091728 Homo sapi
30	430.6	27.0	1925	9	AK091728 Homo sapi
31	430.6	27.0	1960	9	HSA431704 Homo sapi
32	430.6	27.0	2202	9	HSA291712 Homo sapi
33	430.6	27.0	2634	6	AX746908 Sequence
34	430.2	26.9	1311	9	AK091310 Homo sapi
35	430.2	26.9	1311	12	BT007212 Homo sapi
36	429	26.9	1810	9	BT008253 Synthetic
37	429	26.9	2098	9	HSA243488 Homo sapi
38	425.2	26.6	1702	5	CR354317 Gallus ga
39	423.4	26.5	20092	10	AL627253 Mouse DNA
40	390	24.4	531	6	AX313116 Sequence
41	383.8	24.0	1678	5	BC075897 Danio rer
42	374.2	23.4	1500	6	AX060632 Sequence
43	368.4	23.1	1903	9	AF361946 Homo sapi
44	345.8	21.7	1329	9	AF291714 Homo sapi
45	342.2	21.4	1539	5	BC071428 Danio rer

ALIGNMENTS

RESULT 1
AX418852
LOCUS AX418852 1597 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 5 from Patent WO0206318.
ACCESSION AX418852
VERSION AX418852.1 GI:21523716
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1
AUTHORS Olson,E.N. and Spencer,J.A.
TITLE Methods and compositions for stabilizing microtubules and intermediate filaments in striated muscle cells
JOURNAL Patent: WO 0206318-A 5 24-JAN-2002;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
FEATURES
source
1..1597
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
299..1330
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD35457.1"
/db_xref="GI:21523717"
/translation="MDYKSLIPDGNAMENLEKOLICPICLEMFTKPVVILPCORNIC
RKANDITQANPTWNRGVSUSGGRFCPCSCHEVIMDRHGVYGLQRNLLVENII
DIYQECSSRLPQKSGHCKEHEDEKINIYCLTCEVPTCSLCKRVYGAHACEVAPLQ
SIFQCKTELNCISMLVAGNDRVQTIISQLEDCRVTENSHQVKELSQKDFLYA
ILDEKSELRLITQOEKELGFTBALIQVREKLEKTKLVETAIQSLDEPGGATFL
SSAKOLIKSIVEASKGCLGTEQGFENMDYFTLDEHIAEALRAIDFGTGKGDVTC
LTFERQSS"

ORIGIN

Query Match 100.0%; Score 1597; DB 6; Length 1597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CTCGAGATTACCTTACAGAGCTGTTCGGAGGACCTTCCCTTGGCAGCAGCTCAG 60
|||||

Submitted (05-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk
Email: cgaps-xemail.nih.gov

Tissue Procurement: Jeff Green/Paturu Kondaiah, NCI.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W., Teurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 137 Row: 8 Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18266713.

FEATURES
Location/Qualifiers
1..1858
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="MGC:72330 IMAGE:5599072"
/tissue_type="Prostate, pool of NCI_CGAP_Pr30, 40, 41 and NCI_CGAP_Pr29, 39, 42"
/clone_lib="NCI_CGAP_Pr50"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6.1"
1..1858
/gene="Rnf28"
/note="synonyms: Murf, Murf1"
/db_xref="LocusID:140939"
/db_xref="RGD:619964"
82..1137
/gene="Rnf28"
/codon_start=1
/product="ring finger protein 28"
/protein_id="AAH61824.1"
/db_xref="GI:38197350"
/db_xref="LocusID:140939"
/db_xref="RGD:619964"
/translation="MDYKSLIPDGNAMENLEKOLICPICLEMTPKPVILPCOHNLC RKADIPQANPYWTRNGSVSGGRFCPSRCRHEVIMDRHGVYGLQNLVLVLIQ DIYKQESCSPLQKSGHPMCKEHEDEKINITYCLTCEVPTCSLCKVCAHQACEVAPLI SFQKQTELSNCSIMLVAGNDRVQTIISOLESDCRVTKENSHOVKEELSHKFDALV ILDEKSELLQRTQOEKGLDFTBALILQYRQLEKSTKLIVETAKSLDEPGGAFTFL LSKPLTKISVEASNGCOLKTSQGFENMDYFTLNLEHIAELRAIDFGTDEPGGAFTL EEEEDQEEGVSTEGHQ"

ORIGIN
Query Match 57.68; Score 919.4; DB 10; Length 1858;
Best Local Similarity 93.18; Pred. No. 2.9e-203;
Matches 973; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

Qy 253 ACTTGGTGTGACGCGAGCTGGGCAAGACAGTCGCA-TTTTCAAGCAATATGGATTATAAAT 311
|||||
Db 35 ACTCGGTGTGACGCGAGCTGGAGAGACAGTCGCGAGTTTCGAGCAATATGGATTATAAT 94
|||||

Qy 312 CTAGCCTGATTCCTGATGGAAACCGTATGGAGAACTTGGAGAACGACTGATCTGCCCA 371
|||||

Db 95 CTGCTTGATTCCGAGCGGAAATGCTATGAGAACCTTGGAGAACGACTGATCTGCCCA 154
|||||

SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE	1 (bases 1 to 1861)	
AUTHORS	Bodine,S.C., Latres,E., Baumhueter,S., Lai,V.K.-M., Nunez,L., Clarke,B.A., Poueymirou,W.T., Panaro,F.J., Na,E., Dharmarajan,K., Pan,Z.-Q., Valenzuela,D.M., DeChiara,T.M., Stitt,T.N., Yancopoulos,G.D. and Glass,D.J.	
TITLE	Identification of ubiquitin ligases required for skeletal muscle atrophy	
JOURNAL	Science 294 (5547), 1704-1708 (2001)	
MEDLINE	21578247	
PUBMED	11679633	
REFERENCE	2 (bases 1 to 1861)	
AUTHORS	Nunez,L. and Glass,D.J.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-OCT-2001) Muscle Research, Regeneron Pharmaceuticals, 777 Old Saw Mill River Road, Tarrytown, NY 10591, USA	
FEATURES	Location/Qualifiers	
source	1..1861	
	/organism="Rattus norvegicus"	
	/mol_type="mRNA"	
	/strain="Sprague-Dawley"	
	/db_xref="taxon:10116"	
	95..1150	
	/notes="MuRF1; monomeric E3 ubiquitin ligase"	
	/codon_start=1	
	/product="muscle ring finger protein 1"	
	/protein_id="AAL16405.1"	
	/db_xref="GI:16444656"	
	/translation="MDYKSLIPDGNAMENLEKQLICPLEMFTKPVVILPCOHNLC RKCNDIFORANPYNTVSGSVMSGGRFCRSCHREVIMDRHGVQLQRLNLVENII DIYQECRSRPLOKQSHPMCKEHEKINILYCLTCEVPTCSLKVFQGAHACEVAPLO SIYFOQKTELSCINMLVAGNDRVQTIISQLEDSCRVTKENSHVKELSHFKFDALYA ILDEKSELLQRTIQEQLKDFIALILQYREQLKSTKLVTETAIQSLDEPGGATFL LSAKPLIKSIVASKQGLKTEQGFENMDYFTLNLEHIAELRAIDFOTDEEBEFTE EEEEDQESGVSTEGHQ"	
CDS		
ORIGIN		
Query Match	57.5%; Score 917.8; DB 10; Length 1861;	
Best Local Similarity	93.0%; Pred. No. 6.9e-203;	
Matches	972; Conservative 0; Mismatches 72; Indels 1; Gaps 1;	
QY	253	ACTTGTGTGAGCGAGTGGCAAGACACGTCCCA-TTTCAAAGCAATATGGATTATAAT 311
Db	48	ACTCGTGTGAGCGAGGTGGAAGAGACAGTCGCGAGTTTCGAAGCAATATGGATTATAAT 107
QY	312	CTAGCCTGATTCCTGATGGAACCGCTATGGAGAACCTGGAGAACGACGCTGATCTGCCCA 371
Db	108	CTGGCTTGATTCGGACGGAATGCTATGGAGAACCTGGAGAACGCTCATCTGCCCA 167
QY	372	TTGCCTCGAGATGTTTACCAAGCCTGTGCTCATCTGCCCTGCCCAACAACCTCTGCC 431
Db	168	TTGCCTCTGAGATGTTTACCAAGCCTGTGCTCATCTGCCCTGCCCAACAACCTCTGCC 227
QY	432	GGAGTGTGCCAACGACATCTTCCAGGCTCGGATCCCTACTGGACCAACCGGGTGGCT 491
Db	228	GGAAAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTACTGGACCAACCGGGTGGCT 287
QY	492	CAGTGTCCATGCTTGAGGTGCTGTTCCGTTGCCCTCTGCGCGCCATGAAGTGATCATCG 551
Db	288	CGGTGTCATGCTTGAGGTGCTGTTCCGCTGCCCTCTGCGCGCCATGAAGTGATCATCG 347
QY	552	ACCGCAACCGGGTGTACCGCTGACAGAAACCTGCTGGTGGAAACATCATTTGACATCT 611
Db	348	ACCGCATGGGTGTACCGCTGACAGAAACCTGCTGGTGGAAACATCATTCGACATCT 407
QY	612	ACAGCAGAGTGTCTCAGTCGGCCCTCGAGAGGAGCCACCGATGTCGAGGAC 671
Db	408	ACAAGCAGGAATGCTCTCAGTCGGCCCTCGAGAGGAGCCACCGATGTCGAGGAAAC 467
QY	672	ACGAAGACGAGAAGATCAACATCTACTGTCTCA CGTGTGAGGTGCTACTTGTCTCTTGT 731
Db	468	ACGAGACGAGAAATCAACATCTACTGTCTCA CGTGTGAGGTGCTACTTGTCTCTTGT 527
QY	732	GCAAGGTGTTGGGCTCACAGGCTGTGAGGTGCGCCCTTTGGCAAACATCTTCCAAAG 791
Db	528	GCAAGGTGTTGGGCTCACAGGCTGTGAAAGTTGCCCCCTTTACAAAGCATCTTCCAAAG 587
QY	792	GACAGAGACTGAGCTGAGTACTCATCTCTGCTGCTGCTGGTGGGGGAGACGACCGAGTGC 851
Db	588	GACAGAGACTGAACTGAGCAATTGCACTCTCATCTGCTGCTGGCAGGGAACGACCGAGTTC 647
QY	852	AGACCATCATCTCTCAGCTGGAGGACTCTGTCGAGAGTGACCAAGGAGAAATAGCCACAGG 911
Db	648	AGACTATCATCTCGCAGCTGGAGGACTCTCTCGGAGTGACCAAGGAACAGCCACAGG 707
QY	912	TGAAGGAGAGCTGAGTTCAGAAATTTGACACCTCTACGCCATCTCTGGATGAGAAGAAGA 971
Db	708	TGAAGGAGGAACTGAGCCACAAGTTTTCAGCCCTCTTACGCCATCTCTGGACGAGAAGAAGA 767
QY	972	GCGAGCTGCTGCAGCGGATCACGAGGAGCAGGAGGAGAGCTGGGCTTCATCGAGGCTC 1031
Db	768	GTGAGCTGCTGCAGCGGATCACTCAGGAGCAGGAGGAGAGCTGGACTTTCATCGAGGCC 827
QY	1032	TGATCCTCAGTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCCATCC 1091
Db	828	TGATCCTCAGTACCGAGAGCAGTTTGGAAAAGTTCGACCAAGCTTGTGGAAAACAGCCATCC 887
QY	1092	AGTCCCTGATGAGCCCGGAGGGGTACTTCTCTCTCAAGTGCCTCAAGCAGCAGCTCATCAAGA 1151
Db	888	AGTCCCTGATGAGCCCGGAGGGCCACTTCTCTCTTGAGTGCCTCAAGCGCTCATCAAGA 947
QY	1152	GCATTGTAGAAAGCTCCCAAGGCTCCAGCTGGGGAAGACAGCAAGGCTTTGAGAAC 1211
Db	948	GCATTGTAGAAAGCTCCCAAGGCTCCAGCTGGGGAAGACAGCAAGGCTTTGAGAAC 1007
QY	1212	TGGACTACTTTACTCTGCACTTAGAACACATAGCAGAGGCTTTGAGGGCCATTGACTTTG 1271
Db	1008	TGGACTACTTTACTCTGCACTTAGAACACATAGCAGAGGCTTTGAGGGCCATTGACTTTG 1067
QY	1272	GGACAGGTAAGAGTGTGATGTAC 1296
Db	1068	GGACAGATGAGGAGGAGGATTAC 1092
RESULT 4		
HSA291713		
LOCUS	Homo sapiens mRNA for RNF28 gene for ring finger protein 28.	
DEFINITION	HSA291713	
ACCESSION	AJ291713	
VERSION	AJ291713.1 GI:13171050	
KEYWORDS	ring finger protein 28; RNF28 gene.	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
REFERENCE	1	
AUTHORS	Centner,T., Yano,J., Kimura,E., McElhinny,A.S., Pelin,K., Witt,C.C., Bang,M.L., Trombitas,K., Granzier,H., Gregorio,C.C., Sorimachi,H. and Labeit,S.	
TITLE	Identification of muscle specific ring finger proteins as potential regulators of the titin kinase domain	
JOURNAL	J. Mol. Biol. 306 (4), 717-726 (2001)	
MEDLINE	21140140	
PUBMED	11243782	
REFERENCE	2 (bases 1 to 2097)	
AUTHORS	Centner,T.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-FEB-2001) Centner T., Structure and Biocomputing, EMBL-Heidelberg, Meyerhofstrasse 1, Heidelberg 69112, Germany	
REMARK	Revised by author 22-FEB-2001	
FEATURES	Location/Qualifiers	
source	1..2097	

		/protein_id="CAC81706.1"			
		/db_xref="GI:18073356"			
		/db_xref="GOA:Q96901"			
		/db_xref="UniProt/Swiss-Prot:Q96901"			
		/translation="MDYKSLIQDGNPMENLSKQLICPICLEMTFKPVVILPCQHNLC			
		RKANDIFQANPYWTSRGSVSMGSRFCPTCRHEVIMDRHGVVGLQRLNLIVENII			
		DIYQKCSRPLQKSHPMCKHEDEKINIYCLTCEVPTCSMKVFGIHKACEVAPLQ			
		SVFQKQTEILNLCISMLVAGNDRVOTIITQLEDSRRVTKENSHOVKEELSKQFDTLYA			
		ILDEKSELLQRTIQEOKLSFIEALIQQYQOLDKSKLVETATQSLDDEPGATFL			
		LTAKOLIKSIVRASKGCOLGKTEQGFENMDFTLDEHTADALRAIDFTDDEEBEFI			
		EEDQEEESTEGKEBHQ"			
exon		283..455	/gene="MURF2"		
			/number=2		
exon		456..624	/gene="MURF2"		
			/number=3		
exon		625..720	/gene="MURF2"		
			/number=4		
exon		725..954	/gene="MURF2"		
			/number=5		
exon		955..977	/gene="MURF2"		
			/number=6		
exon		978..1102	/gene="MURF2"		
			/number=7		
exon		1103..1174	/gene="MURF2"		
			/number=8		
exon		1175..1756	/gene="MURF2"		
			/number=9		
polyA_signal		1720..1725	/gene="MURF2"		
polyA_site		1756	/gene="MURF2"		
ORIGIN					
Query Match		50.2%;	Score 802.2;	DB 9;	Length 1756;
Best Local Similarity		86.1%;	Pred. No. 5.7e-176;		
Matches 888;		Conservative 0;	Mismatches 143;	Indels 0;	Gaps 0;
QY	262	GACGAGGTGGGCAAGACAGCTGCATTTCAAAGCAATATGGATTATAAATCTAGCCTGAT	321		
DB	87	GAGGCAGCTAGCGTGGCTCTCATTTCCCTCCACAGAATGGATTATAAGTCGAGCCTGAT	146		
QY	322	TCTGTATGGAACGCTATGAGAAACCTGGAGAGCAGCTGATCTGCCCCATCTGCCTGGA	381		
DB	147	CCAGGATGGGAATCCCATGGAGAACTTGGAGAGCAGCTGATCTGCCCTATCTGCCCTGA	206		
QY	382	GATGTTTACAGCCTGTGTGTCATCTGCCCTGCCAACHCAACTCTGCCGGAAGTGTGC	441		
DB	207	GATGTTTACCAAGCAGTGTGTGTCATCTTGCGGTGCCAGCAAACTGTGCCGGAAGTGTGC	266		
QY	442	CAACGACATCTTCAGCGTGGCAATCCCTACTGACCAACCGCGGTGCTCAGTGTCCAT	501		
DB	267	CAATGACATCTTCAGCGTGGCAATCCCTACTGACCAACCGCGGTGCTCAGTGTCCAT	326		
QY	502	GTCTGGAGGTGCTTTCCTGCTGCTGCTGCCCATGAAAGTGATCATGGACCGGACCGG	561		
DB	327	GTCTGGAGGCGTTCCTGCTGCTGCTGCCACCTGCCGCCACGAGGTGATCATGGATCGTCA	386		
QY	562	GGTGTACGGCTGCAGAGGAACCTGCTGGTGGAAACATCATTTGACATCTACAGCAGGA	621		
DB	387	AGTGTACGGCTGCAGAGGAACCTGCTGGTGGGAACATCATCGACATCTACAAACAGGA	446		
QY	622	GTGCTCCAGTCCGCCCTGCAGAAAGCAGCCACCGCATGTGCAAGGAACACCAAGACGA	681		
DB	447	GTGCTCCAGTCCGCCCTGCAGAAAGGCGAGTCACCCCAATGTGCAAGGACGACCAAGATGA	506		

QY	682	GAAGATCAACATCTACTGTCTTCACGTTGTAGGTGCCTACTTGTCTCTTGTGCAAGGTGTT	741			
DB	507	GAATAATCAACATCTACTGTCTTCACGTTGTAGGTGCCCAACCTGCTCCATGTGCAAGGTGTT	565			
QY	742	TGGGGCTCACCAGCGCTGTGAGGTGGCCCTTTTCCAAAGCATCTTCCAAAGCACAGAGAC	801			
DB	567	TGGGATCCACAAGCGCTGCGAGGTGGGCCCAATTGCAGAGTGTCTTCAGGGACAAAAGAC	626			
QY	802	TGAGCTGAGTAACCTGCATCTCCATGCTGGTGGCGGGGAAACGACCGAGTGCAGACGATCAT	861			
DB	627	TGAATGATTAACCTGTATCTCATGCTGGTGGCGGGGAAAGACCGTGTGCAGACCATCAT	686			
QY	862	CTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGAGAAATAGCCACAGGTGAAGAGGAGGA	921			
DB	687	CACCTCAGCTGGAGGATCCCGTGCAGTGCACCAAGGAGAAACAGTCACCCAGGTAAAGGAAGA	746			
QY	922	GCTGAGTCAGAAAGTTTGACACCCCTCTAGCCCATCTCGATGAGAGAGAGAGGAGCGTCTCT	981			
DB	747	GCTGAGCCAGAAAGTTTGACACGTTGTATGCCATCTCGATGAGAAAGAAAGTGAAGTGTCT	806			
QY	982	GCAGCGGATCACGAGGAGCAGGAGGAGAGAGCTGGGCTTCATCGAGGCTCTGTATCTCTCCA	1041			
DB	807	GCAGCGGATCACGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	866			
QY	1042	GTACAGGAGCAGCTGGGAAAGTCCACCAAGCTTTGTGGAGACCGCCATTCAGTCCCTGGA	1101			
DB	867	GTACCAGGAGCAGCTGGGAAAGTCCACCAAGCTTTGTGGAGACCGCCATTCAGTCCCTGGA	926			
QY	1102	TGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1161			
DB	927	CGAGCCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	986			
QY	1162	AGCTTCCAAAGGCTGCCAGCTGGGGAAGACAGAGCAAGGCTTTTGAGAAACATGGAATCTCT	1221			
DB	987	AGCTTCCAAAGGCTGCCAGCTGGGGAAGACAGAGCAAGGCTTTTGAGAAACATGGAATCTCT	1046			
QY	1222	TACTCTGGACTTAGAACAACATAGCAGAGGCGCTTGAGGCGCCATTTGGGACAGGTAA	1281			
DB	1047	TACTTTGGATTTAGAGCACATAGCAGAGCGCCCTGAGAGCCATTTGGGACAGATGA	1106			
QY	1282	AGGATGTGATG 1292				
DB	1107	GGAAGAGGAAG 1117				
RESULT 6		AX274927	1764 bp	DNA	linear	PAT 29-OCT-2001
LOCUS		Sequence 192 from Patent WO0172777.				
DEFINITION		AX274927				
ACCESSION		AX274927.1				
VERSION		GI:16547559				
KEYWORDS		Homo sapiens (human)				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE		1 Hillman, J.L., Baughn, M.R., Yue, H., Lal, P., Lu, D.A., Patterson, C., Azimzai, Y., Bandman, O., Tang, Y.T., Mathur, P., Shah, P., Au-Young, J. and Reddy, R.				
AUTHORS		Transcription factors				
TITLE		Patent: WO 0172777-A 192 04-OCT-2001;				
JOURNAL		Incyte Genomics, Inc. (US)				
FEATURES		Location/Qualifiers				
source		1..1764				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
		/note="Incyte ID No: 3575519CB1"				
ORIGIN						
Query Match		50.2%;	Score 802.2;	DB 6;	Length 1764;	
Best Local Similarity		86.1%;	Pred. No. 5.7e-176;			

QY	682	GAAGATCAACATCTACTGTCTCACGTGTGAGGTGCTACTTGTCTCTTGTGCAAGTGT	741		
DB	507	GAATATCAACATCTACTGTCTCACGTGTGAGGTGCCACCTGCTCCATGTGCAAGTGT	566		
QY	742	TGGGGCTCACAGGCTGTGAGGTGGCCCTTTGCAAGCATCTTCCAAAGACAGAGAC	801		
DB	567	TGGGATCCACAAGGCTGCGAGGTGGCCCCATTTGCAGAGTGTCTTCAGGGACAAGAC	626		
QY	802	TGAGCTGAGTAACTGCATCTCCATGCTGTGTGGCGGGAAACGACCGAGTGCAGACGATCAT	861		
DB	627	TGAATGATAACTGTATCTCATGCTGTGTGGCGGGGAATGACCGTGTGCAGACCATCAT	686		
QY	862	CTCTCAGCTGGAGGACTCGTGCAGAGTGAACCAAGGAGAAATAGCCACAGGTGAAGGAGGA	921		
DB	687	CACTCAGCTGGAGGATTCCTGTCGAGTGACCAAGGAGAAACAGTCAACAGGTAAGGAAGA	746		
QY	922	GCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCTCTGGATGAGAAAGAGCGAGCTGCT	981		
DB	747	GCTGAGCCAGAAAGTTTGACACCGTTGTATGCCATCTCTGGATGAGAAAGAAAGTCAGTGTCT	806		
QY	982	GCAGCGGATCACGACGAGGACGAGGAGAAAGCTGGGCTTTCATCGAGGCTCTGATCTCTCCA	1041		
DB	807	GCAGCGGATCACGACGAGGACGAGGAGAAAGCTGAGTTCATCGAGGCCCTCATCCAGCA	866		
QY	1042	GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTTGTGGAGACGCCATCCAGTCCCTGGA	1101		
DB	867	GTACCAGGAGCAGCTGGACAAGTCCACAAGAGCTGGTGGAAAACCTGCCATCCAGTCCCTGGA	926		
QY	1102	TGAGCCCGAGGGGCTACCTTCTCTCAAGTCCCAAGCAGCTCATCAAGAGCATTTGTAGA	1161		
DB	927	CGAGCCTGGGGAGGCCACCTTCTCTTGTACTGCCAAGCAACTCATCAAAAGCAATTTGGA	986		
QY	1162	AGCCTTCAAGGGCTGCCAGCTGGGGAAGACAGAGCAAGGCTTTGAGAACATTGACTACTT	1221		
DB	987	AGCTTCAAGGGCTGCCAGCTGGGGAAGACAGAGCAGGCGCTTTGAGAACATGACTTCTT	1046		
QY	1222	TACTCTGCACTTAGAACACATAGCAGAGGCGCTTGAGGCGCATTTGTTGGGACAGGTAA	1281		
DB	1047	TACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGCCATTGACTTTGGGACAGATGA	1106		
QY	1282	AGGATGTGATG 1292			
DB	1107	GGAAGAGGAAG 1117			
RESULT 6					
AX274927					
LOCUS					
Sequence 192 from Patent W00172777.					
ACCESSION					
AX274927.1					
VERSION					
KEYWORDS					
SOURCE					
Homo sapiens (human)					
ORGANISM					
Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE					
AUTHORS					
1 Hillman, J.L., Baughn, M.R., Yue, H., Lal, P., Lu, D.A., Patterson, C.,					
Azimzai, Y., Bandman, O., Tang, Y.T., Mathur, P., Shah, P., Au-Young, J.,					
and Reddy, R.					
Transcription factors					
Patent: WO 0172777-A 192 04-OCT-2001;					
Incyte Genomics, Inc. (US)					
FEATURES					
source					
1..1764					
/organism="Homo sapiens"					
/mol_type="unassigned DNA"					
/db_xref="taxon:9606"					
/note="Incyte ID No: 3575519CB1"					
ORIGIN					
Query Match 50.2%; Score 802.2; DB 6; Length 1764;					
Best Local Similarity 86.1%; Pred. No. 5.7e-176;					

gene	/db_xref="taxon:9606"	
	/clone="MGC:99548 IMAGE:4862321"	
	/tissue_type="Skin, melanotic melanoma, high MDR."	
	/clone_lib="NIH MGC 49"	
	/lab_host="DH10B-R"	
	/note="Vector: pOTB7"	
	1. .1764	
	/gene="RNF28"	
	/notes="synonyms: SMRZ, IRF, FLJ32380, MURF2, MURF1"	
	/db_xref="LocusID:84676"	
CDS	/db_xref="MIM:606131"	
	119. .1180	
	/gene="RNF28"	
	/codon_start=1	
	/product="muscle specific ring finger protein 1"	
	/protein_id="AAH80529.1"	
	/db_xref="GI:51593349"	
	/db_xref="LocusID:84676"	
	/db_xref="MIM:606131"	
	/translation="MDYKSLIQDGNPMENLEKQLICPICLEMTFKPVVILPCOHNLC RKCANDIFOANPYMTSRGSSVSMGGRFCPTCRHEVIMDRHGVYGLORNLIVENII DIYKQCSSRPLQKSGHPMCKEHEDEKINIYCLTCRVPTCSMKVFGIHKACEVAPLQ SVFQCKTELNNCISMLVAGNDRVQTIIQLEDSRRVTAKENSHQVKELSQKFDITLYA ILDEKSELLQRTIQOEKKLSFIEALIQQOYQOLDKSTKLIVETAIQSLDEPGGATFL LTAQLIKISIVASKGCOLGKTEQGFENMDFTLDEHTADALRAIDFGTDEEBEEFI EBEDQEBEESTGKEBHQ"	
ORIGIN		
Query Match 50.2%; Score 802.2; DB 9; Length 1764;		
Best Local Similarity 86.1%; Pred. No. 5.7e-176;		
Matches 888; Conservative 0; Mismatches 143; Indels 0; Gaps 0;		
QY	262	GAGCGAGGTGGGCAAGACATGCGCATTTCAAGCAATATGATTATAAATCTAGCCCTGAT 321
DB	82	GAGCGAGCTAGGCGTGCTCTCATTCCTTCCACAGATGGATTATAGTCGAGCCTGAT 141
QY	322	TCCTGATGGAACCGCTATGAGAACCTGGAGAGCAGCTGATCGCCCATCTGCGCTGGA 381
DB	142	CCAGGATGGAAATCCCATGGAGAACTGGAGAGCAGCTGATCGCCCTATCTGCGCTGA 201
QY	382	GATGTTTACCAAGCCTGTGTCATCTGCTGCTGCCAACAACCTCTGCGGAGTGTGC 441
DB	202	GATGTTTACCAAGCAGTGTGTCATCTGCGTGCAGCAACCTGTGCGGAGTGTGC 261
QY	442	CAACGACATCTTCAGGCTGCGAATCCCTACTGGACCAACCGGGTGGCTCAGTGTCAT 501
DB	262	CAATGACATCTTCAGGCTGCAAAATCCCTACTGGAACCGGGCAGCTCAGTGTCAT 321
QY	502	GTCGAGGTGCTTTTCGTTGCCCTCGTGCGCCCATGAAGTATCATGGAACGGCAGCG 561
DB	322	GTCGAGGCGGTTTTCGCTGCGCCACCTCGCCGACGAGTGTATCATGGATCGTCACGG 381
QY	562	GGTGTACGGCTCGCAGAGGAACCTGCTGGTGGAAACATCATGATCTACAAGCAGGA 621
DB	382	AGTGTACGGCTCGCAGAGGAACCTGCTGGTGGAGAACATCATGCATCTACAAACAGGA 441
QY	622	GTGCTCAGTCGCGCCCTCGAGAAAGCAGCCACCGAGTGTGCAAGAAACAGCAAGACA 681
DB	442	GTGCTCAGTCGCGCGCTCGAGAAAGGAGTGTGCAAGAAAGCAGCAAGATGA 501
QY	682	GAAGATCAACATCTACTGTCTCAGTGTGAGGTGCTTCTGCTCTTGTGCAAGGTGTT 741
DB	502	GAAGATCAACATCTACTGTCTCAGTGTGAGGTGCTTCTGCTCTTGTGCAAGGTGTT 561
QY	742	TGGGGCTCACACGGCTGTGAGGTGCTTCTTTCGAAAGCATCTTCCAGGACAGCAAGAC 801
DB	562	TGGGATCCAAAGGCTGTGAGGTGCTTCTTTCGAGAGTGTCTTCCAGGACAGCAAGAC 621
QY	802	TGAGCTGAGTAACTGCATCTCCATGCTGTTGGCGGGAAACGACCGAGTCAGACATCAT 861
DB	622	TGAACTGAATTAATCTGATCTCCATGCTGTTGGCGGGGAATGACCGTGTGAGACCATCAT 681
QY	862	CTCTCAGCTGGAGGACTCGTGCAGAGTGAACCAAGGAGAAATAGCCACCAAGGTGAAGAGGA 921

DB	682	CACTCAGCTGGAGGATTCCTCGTGCAGTGACCAAGGAGAACAGCTCACCCAGGTAAAGGAGA 741
QY	922	GCTGAGTCAGAAGTTTGACACACCTCTACGCCATCTCGGATGAGNAGAGGAGCGAGTCTCT 981
DB	742	GCTGAGCCAGAAAGTTTGACACACCTCTATGCCATCTCGGATGAGNAGAGGAGGAGTCTCT 801
QY	982	GCAGCGGATCAGCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1041
DB	802	GCAGCGGATCAGCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 861
QY	1042	GTACAGGAGCAGCTGGAAGAAAGTCCACCAAGCTTGTGGAGAGCGGCATCCAGTCCCTGGA 1101
DB	862	GTACAGGAGCAGCTGGAAGAAAGTCCACCAAGCTTGTGGAGAGCGGCATCCAGTCCCTGGA 921
QY	1102	TGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1161
DB	922	CGAGCGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 981
QY	1162	AGCCTCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1221
DB	982	AGCTTCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1041
QY	1222	TACTCTGGAAGCTTAGAACACATAGCAGAGCGCTTGGAGGCGCATTGATTTGGGAGCAGGTA 1281
DB	1042	TACTTGGATTTAGAGCACATAGCAGAGCGCTTGGAGGCGCATTGATTTGGGAGCAGATGA 1101
QY	1282	AGGATGTGATG 1292
DB	1102	GGAAGAGGAAG 1112
RESULT 8		
AF353673		
LOCUS		
DEFINITION Homo sapiens iris ring finger protein mRNA, complete cds.		
ACCESSION AF353673		
VERSION AF353673.1 GI:13785923		
KEYWORDS		
SOURCE Homo sapiens (human)		
ORGANISM		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE 1 (bases 1 to 1791)		
AUTHORS Wistow,G.		
TITLE IRF: A Novel Ring Finger Protein From Iris		
JOURNAL Unpublished		
AUTHORS 2 (bases 1 to 1791)		
Wistow,G.		
TITLE Direct Submission		
JOURNAL Submitted (27-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD 20892, USA		
FEATURES		
source		
1. .1791		
/organism="Homo sapiens"		
/mol_type="mRNA"		
/db_xref="taxon:9606"		
/chromosome="1"		
/map="1p33-p31"		
/tissue_type="iris"		
120. .1181		
/note="IRF"		
/codon_start=1		
/product="iris ring finger protein"		
/protein_id="AAK39519.1"		
/db_xref="GI:13785924"		
/translation="MDYKSLIQDGNPMENLEKQLICPICLEMTFKPVVILPQHNLC RKCANDIFOANPYMTSRGSSVSMGGRFCPTCRHEVIMDRHVVYGLORNLIVENI DIYKORCSSRPLQKSHPMCKSHEDKINIYCLTCRVPTCSMKVFGIHKACEVAPLQ SVFQCKTELNNCISMLVAGNDRVQTIIQLEDSRRVTAKENSHQVKELSQKFDILYA ILDEKSELLQRTIQOEKKLSFIEALIQQOYQOLDKSTKLIVETAIQSLDEPGGATFL LTAQLIKISIVASKGCOLGKTEQGFENMDFTLDEHTADALRAIDFGTDEEBEFI EBEDQEBEESTGKEBHQ"		
CDS		

ORIGIN

Query Match 50.1%; Score 802.2; DB 9; Length 1791;
Best Local Similarity 86.1%; Pred. No. 5.7e-176;
Matches 888; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 262 GACGAGGTGGCAGACAGTGGCATTTTCAAGCAATATGGATTATTAATCTAGGCTGAT 321
DB |||||
QY 83 GAGGAGCTAGGCGTGGCTCTCATTCCTTCCACAGAATGGAATTAAGTCGAGCTGAT 142
DB |||||
QY 322 TCCTGATGAACGCTATGGAGAACCTGGAGAACGCTGATCTGCCCATCTGCTCGA 381
DB |||||
QY 143 CCAGATGGGAATCCATGGAGAACTTGGAGAACGCTGATCTGCCCATCTGCTCGA 202
DB |||||
QY 382 GATGTTTACCAGCCTGTGGTCACTCTGCCCTGCCAACACACACCTCTGCCGAAGTGTGC 441
DB |||||
QY 203 GATGTTTACCAGCCAGTGTCTCATCTGCCGTGCCAGCACACCTGTGCCGAAGTGTGC 262
DB |||||
QY 442 CACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGCGGTGGCTAGTGTCCAT 501
DB |||||
QY 263 CAATGACATCTTCCAGGCTGCAATCCCTACTTGGACCAACCGCGGCGAGCTCAGTGTCCAT 322
DB |||||
QY 502 GTCTGGAGTGTGTTCCGTTGCCCTCGTGGCCGCAATGAAGTATCATGGACCGGACGG 561
DB |||||
QY 323 GTCTGGAGCGCTTTCGCTGCCCACTGCCGCCAGAGGTGATCATGGATCGTCACGG 382
DB |||||
QY 562 GGTGTACCGCCTGCAGAGGAACCTGCTGGTGGAAACATCATTTGACATCTTCAACAGCAGA 621
DB |||||
QY 383 AGTGTACGGCCTGCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTACAAACAGA 442
DB |||||
QY 622 GTGCTCCAGTGGCCCTGCAGAAAGGAGCGCACCCGATGTGCAAGGAAACAGAAAGCA 681
DB |||||
QY 443 GTGCTCCAGTGGCCCTGCAGAGGCGAGTCACTCCATGTGCAAGGAGCACCAAGATGA 502
DB |||||
QY 682 GAAGATCAACATCTACTGCTCACTGTGAGGTGCTACTTCTCTTGTGCAAGGTCTT 741
DB |||||
QY 503 GAAATCAACATCTACTGCTCACTGTGAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCT 562
DB |||||
QY 742 TGGGCTCACCAGGCTGTGAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 801
DB |||||
QY 563 TGGGATCCACAAGGCTTGGAGGTGGCCCATTTGCAGAGTGTCTTCCAGGACAAAGAC 622
DB |||||
QY 802 TGAGCTGAGTAATCGATCTCATCTGCTGGTGGCGGGGAAAGCAAGAGTGCAGACATCAT 861
DB |||||
QY 623 TGAATGAATAACTGTATCTCATCTGCTGGTGGCGGGAATGACCGGTGTGACACCATCAT 682
DB |||||
QY 862 CTCTCAGTGGAGGACTGTGACAGTGCACCAAGGAGATAGCCACAGGTGAAGGAGA 921
DB |||||
QY 683 CACTCAGCTGGAGGATTTCCCGTGGAGTGAACCAAGGAGAACAGTCAACAGGTAAAGGAGA 742
DB |||||
QY 922 GCTGAGTCAGAGTGTGACACCTCTAGCCCATCTCTGATGAGAAAGAGAGCGAGCTGCT 981
DB |||||
QY 743 GCTGAGCCAGAGTTTGACACGTTGTATGCCATCTCTGATGAGAAAGAGTGTGCT 802
DB |||||
QY 982 GCAGCGGATTCAGCAGGAGCAGGAGAGAGTGGGCTTTCATCGAGGTCTGATCCTCCA 1041
DB |||||
QY 803 GCAGCGGATTCAGCAGGAGCAGGAGAGAGTGGGCTTTCATCGAGGCTTTCATCCAGCA 862
DB |||||
QY 1042 GTACAGGAGCAGCTGGAGAAAGTCCACCAAGCTTGTGGAGCCGATCCAGTCCCTGGA 1101
DB |||||
QY 863 GTACAGGAGCAGCTGGAGAAAGTCCACCAAGCTTGTGGAGAACTGCGCATCCAGTCCCTGGA 922
DB |||||
QY 1102 TGAGCCCGAGGGGCTTACCTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATTTGTAGA 1161
DB |||||
QY 923 CGAGCCTGGGGAGGCCATCTTCTTGTACTGCCAGGCACTCATCAAAAGCATTTGTGA 982
DB |||||
QY 1162 AGCCTCCAGGGCTGCCAGTGGGAGAGCAGAGCAAGGCTTTTGAGAAATGGAATGACTT 1221
DB |||||
QY 983 AGCTTCCAGGGCTGCCAGCTGGGAGAGCAGAGCAGGAGGCTTTTGAGAAATGGAATGACTT 1042
DB |||||
QY 1222 TACTCTGAGCTTAGAACAATAGCAGAGGCTTTGAGGGCCATTTGAGGAGCAGGATA 1281
DB |||||
QY 1043 TACTTTGGATTTAGAGCAATAGCAGAGCGCCCTGAGAGCATTTGAGGAGCATTTTGGACAGATGA 1102
DB |||||

QY 1282 AGGATGTGATG 1292
DB 1103 GGAAGAGGAAG 1113

RESULT 9
AX714538
LOCUS AX714538 1764 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 1222 from Patent EP1293569.
ACCESSION AX714538
VERSION AX714538.1 GI:29889491
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahara,K. and Masuho,Y.
TITLE Full-length cDNAs
JOURNAL Patent: EP 1293569-A 1222 19-MAR-2003;
Helix Research Institute (JP) ; Research Association for Biotechnology (JP)
FEATURES
source
1. 1764
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 50.1%; Score 800.6; DB 6; Length 1764;
Best Local Similarity 86.0%; Pred. No. 1.4e-175;
Matches 887; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 262 GACGAGGTGGGCAAGACAGTGGCATTTTCAAGCAATATGGATTATTAATCTAGGCTGAT 321
DB |||||
QY 100 GAGGAGCTAGGCGTGGCTCTCATTCCTTCCACAGAATGGATTATAAGTCGAGCTGAT 159
DB |||||
QY 322 TCCTGATGGAACGCTATGGAGAACCTGGAGAACGAGTGTCTGCCCATCTGCTCGA 381
DB |||||
QY 160 CCAGATGGGAATCCCATGGAGAACTTGGAGAACGAGTGTCTGCCCATCTGCTCGA 219
DB |||||
QY 382 GATGTTTACCAGCCTGTGCTCTGCCCTGCCCAACACACCTCTGCCGAAGTGTGC 441
DB |||||
QY 220 GATGTTTACCAGCCAGTGGTCACTTCTGCCGTGCCAGCACACCTGTGCCGAAGTGTGC 279
DB |||||
QY 442 CAAACGACATCTTCCAGGCTGGGAATCCCTACTTGGACCAACCGCGGTGGCTCAGTGTCCAT 501
DB |||||
QY 280 CAATGACATCTTCCAGGCTGCAAAATCCCTACTTGGACAGCCGCGGCGAGCTCAGTGTCCAT 339
DB |||||
QY 502 GTCTGAGGTGCTTTCGTTGGCCCTCTGTCGCCCATGAAGTATCATGGACCGGACGG 561
DB |||||
QY 340 GTCTGAGGCGCTTTCGCTGCCCACTGCCGCAAGAGGTGATCATGGATTCGTCACGG 399
DB |||||
QY 562 GGTTTACGCGCTGCAGAGGAACCTGCTGGTGGAAACATCATTTGACATCTACAAGCAGA 621
DB |||||
QY 400 AGTTTACGCGCTGCAGAGGAACCTGCTGGTGGAGAACATCATTCGACATCTCAAAACAGA 459
DB |||||
QY 622 GTGCTCCAGTGGCCCTTGCAGAAAGGAGCGCACCCGATGTGCAAGGAAACAGAAAGCA 681
DB |||||
QY 460 GTGCTCCAGTGGCGCTGCGAGAGGCGAGTCACCCCATGTGCAAGGAGCAGCAAGATGA 519
DB |||||
QY 682 GAAGATCAACATCTACTGCTCACTGTGAGGTGCTTCTCTCTCTCTCTCTCTCTCTCTCT 741
DB |||||
QY 520 GAAATCAACATCTACTGCTCACTGTGAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 579
DB |||||
QY 742 TGGGCTCACCAGGCTGTGAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 801
DB |||||
QY 580 TGGGATCCACAGGCTTGGAGGTGGCCCATTTGACAGATGTCTTCCAGGGGCAAAAGAC 639
DB |||||

QY 802 TGAGCTGAGTAAGTATGCTATCTCCATGCTGTGGGGGAAACGACCGAGTGCAGACGATCAT 861
|||
Db 640 TGAAGTGAATAAATGATATCTCCATGCTGTGGCGGGAATGACCGTGTGCAGACCATCAT 699
|||
QY 862 CTCTCAGCTGGAGAGCTGTGCAGAGTGCACCAAGGAGATAGCCACAGGTGAAGGAGGA 921
|||
Db 700 CACTCAGCTGGAGGATTCCTCGTGCAGTGACCAAGGAGAAACAGTCCACGAGTAAAGGA 759
|||
QY 922 GCTGAGTGCAGAGTTTGCACACCTCTACGCGCATCTCTGGATGAGAGGAGCGAGCTGCT 981
|||
Db 760 GCTGAGCCAGAGTTTGCACAGTTGTATGCCATCTCTGGATGAGAGAAAGTGTGCT 819
|||
QY 982 GCAGCGGATCACGAGGAGCAGAGGAGAGCTGGGCTTCATCGAGGCTCTGTATCTCTCA 1041
|||
Db 820 GCAGCGGATCACGAGGAGCAGAGGAGAAAGCTTAGCTTCATCGAGGCTCTCATCCAGCA 879
|||
QY 1042 GTACAGGAGCAGCTGAAAAGTCCACCAAGCTTGTGGAGACCGCATTCAGTCCCTGGA 1101
|||
Db 880 GTACACGAGGAGCAGCTGGCAAGTCCCAAGAGCTGGTGGAACTGCCATCCAGTCCCTGGA 939
|||
QY 1102 TGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCACAGCAGCTCATCAAGAGCAATCTGAGA 1161
|||
Db 940 CGAGCTCTGGGAGCCACCTTCTCTTGTACTGCAAGCAACTCATCAAGCAATTTGGGA 999
|||
QY 1162 AGCTTCCAAAGGCTGCGAGCTGGGGAAGACAGACGAGGCTTTTGAGAACATGGACTACTT 1221
|||
Db 1000 AGCTTCCAAAGGCTGCGAGCTGGGGAAGACAGACGAGGCTTTTGAGAACATGGACTTCT 1059
|||
QY 1222 TACTCTGGACTTAGACACATAGCAGAGGCTTGAGGGCCATTTGACTTTGGGACAGGTA 1281
|||
Db 1060 TACTTTGGATTAGACACATAGCAGAGGCTTGAGAGCCCTGAGAGCCATTTGCTGGGACAGATGA 1119
|||
QY 1282 AGGATGTGATG 1292
|||
Db 1120 GGAAGAGGAAG 1130
|||

RESULT 10
AK056942
LOCUS
DEFINITION Homo sapiens cDNA FLJ32380 fis, clone SKMUS1000064, moderately similar to Mus musculus RING-finger protein MURF mRNA.
ACCESSION AK056942
VERSION AK056942.1 GI:16552479
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohtsuka, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, K., Chiba, Y., Iehida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoshida, M., Hottuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotaake, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, K., Kawabata, A., Hiki, J., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,

Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isegai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
2
Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isegai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 1764)
Isegai, T., Otsuki, T. and Sugiyama, T.
Direct Submission
Submitted (24-OCT-2001) Takao Isegai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.
Location/Qualifiers
1. .1764
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SKMUS1000064"
/tissue_type="skeletal muscle"
/clone_lib="SKMUS1"
/note="cloning vector: pME18SFL3"
137. .1198
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB71318.1"
/db_xref="GI:16552480"
/translation="MDYKSLIQDGNPMENLEKQICPICLEMFVKPVVILPCQHNLC RKANDIFQANPNYVTSRGSVSPKCKHEDEKINICLTCEVPTCSCKVGIHKEVAPLQ DIYQECSSRPLOKSGHPMKHEDEKINICLTCEVPTCSCKVGIHKEVAPLQ SVFQOKTELNNICISMLVAGNDRVOTITQLEDSRVTKENSHVKEESUQKRPDTUYA ILDEKSELLORTIOEQKKLSFIALIQOYQDLKSTKVLVETQSLDPEPGATFL LTAQLIKSIVKASGCGQLKTEQGFENMDFFTLDEHTADALRAIDFGTDEEEEF EEDQEEESTEGKEGQ"

FEATURES
source
Query Match 50.1%; Score 800.6; DB 9; Length 1764;
Best Local Similarity 86.0%; Pred. No. 1.4e-175;
Matches 887; Conservative 0; Mismatches 144; Indels 0; Gaps 0;
QY 262 GACGAGGTGGGCAAGACATCGCATTTTCAAAGCAATATGGATTATAAATCTAGCCTGAT 321
|||
Db 100 GAGGAGCTAGCGGTGGCTCTCATCTCTCCACAGATGGATTATAGTCGAGCCTGAT 159
|||
QY 322 TCCTGATGAAACGCTATGAGAACTGAGAGAGCAGCTGATCTGCCCATCTGCTCGGA 381
|||
Db 160 CCAGGATGGAATCCATGAGAACTTGGAGAGCAGCTGATCTGCCCATCTGCTCGGA 219
|||
QY 382 GATGTTTACCAAGCCTGTGTGTCATCTGCCCTGCCACACAACCTCTGCCGGAAGTGTGC 441
|||
Db 220 GATGTTTACCAAGCCTGTGTGTCATCTGCCCTGCCGGAAGTGTGC 279
|||

Db 301 ATCATGCACATCTTACAAACAGGAGTGTCTCCAGTCCGCGCTGCAGAAAGGCGAGTCACCC 360
Qy 659 ATGTGCAAGGAACACGACGACGAGAGATCAACATCTACTGTCTTACGTGTGAGGTGCT 718
Db 361 ATGTGCAAGGAGACGACGAGATGAGAAATCAACATCTACTGTCTTACGTGTGAGGTGCC 420
Qy 719 ACTTGTCTCTTGTGCAAGGTGTTGGGCTCACAGGCTGTGAGGTGTGCCCTTTGCAA 778
Db 421 ACTTGTCTTGTGCAAGGTGTTGGATCCCAAGGCTGTGAGGTGTGCCCTTTGCGAG 480
Qy 779 AGCATCTTCCAGGACAGAGACTGAGCTGAGTAACTGCACTCTTCCATCTGCTGTGGCGGG 838
Db 481 AGTGTCTTCCAGGACAAAGACTGAATGAATTAATGTATCTCCATCTGCTGTGGCGGG 540
Qy 839 AACGACCGAGTGCAGAGATCATCTCTCAGCTGGAGACTGTGCGAGAGTGAACAGGAG 998
Db 541 AATGACCGTGTGCAGACCATCATCATCTAGCTGGAGGATTCGCGTGCAGTGAACAGGAG 600
Qy 899 AATAGCCACAGGTGAAGGAGGAGCTGAGTCAAGTGTGACACCTCTTACGCCATCTCTG 958
Db 601 AACAGTCAACAGGTAAAGNAGAGCTGAGCCAGAGTTTGACACGTTGTATGCCATCTCTG 660
Qy 959 GATGAGAAGAGCAGAGCTGTGCGAGCGGATCACGACGAGCAGGAGAGAGCTGGCG 1018
Db 661 GATGAGAAGAAAGTGAAGTGTCTGCGAGCGGATCACGACGAGCAGGAGGAAAGCTTAGC 720
Qy 1019 TTATCATCGAGCTGTGATCTCTCAGTACAGGAGCAGCTGGAAGTCCACCAAGCTTTG 1078
Db 721 TTATCATCGAGCCCTCATCTCAGCAGTACACGAGGAGCAGTGGACAAGTCCACAAGCTGG 780
Qy 1079 GAGACCGCATTCAGTCCCTGTGATGAGCCGAGGAGGCTACCTTCTCTCAAGTGCCAA 1138
Db 781 GAACTGCCATCAGTCCCTTGAGAGCTGTGGGAGGCCACCTTCTCTTGTACTGCCAAG 840
Qy 1139 CAGCTCATCAAGAGCATTTGAGAGCTTCAAGGCTTCAAGGCTGCGAGTGGGGAAGACAGCAA 1198
Db 841 CAACTCATCAAAAGCATTTGGAAGCTTCCAAGGCTGCGAGTGGGGAAGACAGAGCAG 900
Qy 1199 GCGTTTGAAGACATGACTACTTCTTCTGACTTGAACATAGACAGAGGCTTGAGG 1258
Db 901 GCGTTTGAAGACATGACTTCTTCTTCTTGGATTTTGAAGACATAGACAGCGCTTGAGA 960
Qy 1259 GCCATTGACTTTGGGACAGGTAAGATGTGATGTT 1294
Db 961 GCCATTGACTTTGGGCGAGCTGAAGATGAGAT 996

RESULT 12
BT008198
LOCUS
DEFINITION
BT008198
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
BT008198 1041 bp mRNA linear SYN 13-MAY-2003
Synthetic construct Homo sapiens ring finger protein 28 mRNA,
partial cds.
BT008198
BT008198.1 GI:30585234
FLI CDNA.
synthetic construct
synthetic construct
Other sequences; artificial sequences.
1 (bases 1 to 1041)
Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Cloning of human full-length cDNAs in BD Creator (TM) System Donor
vector
Unpublished
2 (bases 1 to 1041)
Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission
Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA

COMMENT
This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion (TM)
cloning system between the Sali and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sali site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
Location/Qualifiers
1..1041
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="GH000131.1.0"
/clone_lib="BD Creator (TM) CDS Library derived from MGC
collection"
/lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
1..>1041
/note="Mutations: 1040:Stop->Leu"
/codon_start=1
/transl_table=11
/product="Homo sapiens ring finger protein 28"
/protein_id="AAP36890.1"
/db_xref="GI:30585235"
/translation="MDYSSLIQDGNPMENLEKQLICPLEMFTKPVVILPCQHNLC
RKANDIFQANPYWTSRGSVSMGGRPCRTCHREVTIMDRHGVTLGRLNLIVENII
DIYCESSRPLQKSHPMCKHEDEKINIYCLTCEVPTCSMKVFGIHKAEVAPLQ
SYFOQKTLNNCI SMLVAGNDVOTIITQLEDSSRVTKENSHVKEILSKQFDTLYA
ILDEKSKELLORITQOEKLSFIEALIQOYQOLDKSTKLVTETAIQSLDEPGATFL
LTAKOLIKSIVEASKGCLGKTEQGFENMDFTLDEHLADALRAIDFGAAEDDEDD
VDTKQKQYDEDDL"
ORIGIN
Query Match 50.0%; Score 799.2; DB 12; Length 1041;
Best Local Similarity 87.7%; Pred. No. 2.8e-175;
Matches 873; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
Qy 299 ATGGATTATAAATCTAGCCTGATTTCTGATGAAACGCTATGAGAACCTGGAGAACGAG 358
Db 1 ATGGATTATAAGTCAGCGCTGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAACGAG 60
Qy 359 CTGATCTGCCCATCTGCTCGAGAGATGTTTACCAAGCCTGTGTCATCTCGCTGCCCAA 418
Db 61 CTGATCTGCCCATCTGCTCGAGAGATGTTTACCAAGCAGTGTGTCATCTTCGCTGCCAG 120
Qy 419 CACAACCTCTGCCGAAGTGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACC 478
Db 121 CACAACCTGTGCGGAAGTGTGCCAATGACATCTTCCAGGCTGCAATCCCTACTGGACC 180
Qy 479 AACCGGCTGTGCTCAGTGTCCATGTCTGAGAGTGTTCGCTTGCCTTGCCTTGCCTCCAT 538
Db 181 AGCCGGGCGAGCTCAGTGTCCATGTCTGAGGCGCGTTTCCGCTGCCCCACCTGCCGCCAC 240
Qy 539 GAAGTGATCATGACCGCGCGGCTGTACGCGCTGCAGAGGAACCTGCTGTGGGAAAC 598
Db 241 GAGGTGATCATGATGCTGTCAGGAGTGTACGCGCTGCAGAGGAACCTGCTGTGGGAAAC 300
Qy 599 ATCATTGACATCTACAAGCAGGAGTGTCTCAGTCCGCGCTTGCAGAAAGGAGCCACCCG 658
Db 301 ATCATCGACATCTACAAACAGGAGTGTCTCCAGTCCGCGCTGCAGAAAGGAGTCAACCC 360
Qy 659 ATGTGAGGAACACGACGAGACGAGATCAACATCTACTGTCTCAGTGTGAGGTGCT 718
Db 361 ATGTGCAAGGACGACGAGATGAGAAATCAACATCTACTGTCTCAGTGTGAGGTGCC 420
Qy 719 ACTTGTCTCTTGTGCAAGGTGTTGGGCTCACAGGCTGTGAGGTGTGCCCTTTGCAA 778
Db 421 ACTTGTCTTGTGCAAGGTGTTGGATCCCAAGGCTGTGAGGTGTGCCCTTTGCGAG 480
Qy 779 AGCATCTTCCAGGACAGAGACTGAGTAACTGCACTCTTCCATCTGCTGTGGCGGG 838

Db	481	
----	-----	--

Db	268	CAATGATATTTTCCAGGCTCTAAACCGTATTTTGGCCCAAGAGGAGGTACCAACCATGCG	327
Qy	502	GTCTGAGGTGTTTCCCTTGCCTCTGTCGCGCATGAAGTGATCATCGACGGCAGCG	561
Db	328	ATCAGGGGGCCGATTCCTGCTGCCCATCTGTAGACATGAAGTGGTTTGGATAGCATGG	387
Qy	562	GGTGTACGGCTGTCAGAGGAACTCTGCTGGTGGAAACATCATTTGACATCTCAAGCAGGA	621
Db	388	GGTATATGGACTTCAGAGGAACTCTGCTGGTGGAGAACATCATCGACATCTCAAAACAGGA	447
Qy	622	GTGCTCAGTTCGGCCCCCTGTCAGAAAGGAGCAGCCACCGGATGTGCAAGGAACACGAAGACCA	681
Db	448	GTGCTCAGTTCGGCCCCCTGTCAGAAAGGAGCAGTCAACCCATGTGTCAGAGGAGCAGCAAGATGA	507
Qy	682	GAAGATCAACATCTACTGCTCAGCTGTGAGGTGCTTACTTCTCTCTTGTGCAAGGTGTT	741
Db	508	GAAGATCAACATCTACTGCTCAGCTGTGAGGTGCTTACTTCTCTCTTGTGCAAGGTGTT	567
Qy	742	TGGGCTCACCAGGCTGTGAGGTGGCCCCCTTTGCAAGAGCATCTTCCAGAGGACAGAAAGAC	801
Db	568	TGGGATCCACAAGGCTTCGAGGTGGCCCCATTTGCAGAGTGTCTTCCAGGGACAAAAGAC	627
Qy	802	TGAGCTGAGTAACTCATCTCTCATGCTGTGTCGGGGGAAACGACCGAGTGCAGACGATCAT	861
Db	628	TGAACCTGAATAACTGTATCTCCATGCTGTGTCGGGGGAAATGACCGTGTGCAGACCATCAT	687
Qy	862	CTCTCAGCTGAGGAGCTCTGTCAGAGTGCACCAAGGAGAAATAGCCACAGGTGCAAGGAGGA	921
Db	688	CACCTCAGCTGAGGAGTTCCTGTCAGTGCACCAAGGAGAAACAGTCAACAGGTAAAGGAGGA	747
Qy	922	GCTGAGTCAAGAGTTTGCACCCCTCTACGCCATCTCTGATGAGAAAGAGAGGAGCTGCT	981
Db	748	GCTGAGCCAGAAGTTTGCACCGTTGTATGCCATCTCTGATGAGAAAGAGTGTGCT	807
Qy	982	GCAGCGATCAAGGAGGAGGAGAGAGCTGGGCTTTCATCGAGGCTCTGATCTCTCA	1041
Db	808	GCAGCGATCAAGGAGGAGGAGAGAGAGCTTCTGATGAGAAAGAGTGTGCT	867
Qy	1042	GTACAGGAGGAGCTGGAAGAGTCCCAAGCTTGTGAGAGCCGACATCCAGTCCCTGGA	1101
Db	868	GTACAGGAGGAGCTGGAAGAGTCCCAAGCTTGTGAGAGCTGGAAGTGTGCTGGA	927
Qy	1102	TCAGCCCGAGGGCTACCTTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATTTGTAGA	1161
Db	928	CGAGCTTGGGGAGGCCACTTCTCTGACTGCCAAGCAACTCATCAAAAGCATTTGTGA	987
Qy	1162	AGCTTCAAGGGCTGCCAGCTGGGGAGACAGAGCAAGGCTTTGAGACATGGACTACTT	1221
Db	988	AGCTTCAAGGGCTGCCAGCTGGGGAGACAGAGCAGGGCTTTGAGAACATGGACTTCTT	1047
Qy	1222	TACTCTGAGCTTAGAACACATAGCAGAGGCTTTGAGGGCATTGTGCTTTGGGACAGGTA	1281
Db	1048	TACTTTGATTTAGAGCACATAGCAGAGCCCTGAGAGCCATTGACTTTGGGACAGATGA	1107
Qy	1282	AGGATGTGATG 1292	
Db	1108	GGAAGAGGAG 1118	
RESULT 14			
AX576231			
LOCUS	AX576231	2110 bp	DNA linear PAT 08-JAN-2003
DEFINITION	Sequence 12 from Patent WO0162922.		
ACCESSION	AX576231		
VERSION	AX576231.1 GI:27645982		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1		
	Banville, S.C., Greenawalt, L.B., Lincoln, S.E., Stockdrehner, T.K.,		

Amshey,S., Chang,S.C., Chen,W., Dam,T.C., Liu,T.F., Rosen,B.H.,
Russo,F.D., DiSa,S.A., Spiro,P.A., Bradley,D.L., Chen,A.,
Cohen,H.J., Daffo,A., Daniels,S.E., Dufour,G.E., Flores,V.,
Fong,W.T., Hodgson,D.M., Jackson,S., Jones,A.L., Panzer,S.R.,
Roseberry,A.M., Shah,P., Wright,R.J., Yap,P.E., Yu,J.Y.,
Bratcher,S.R., Chalup,M.S., Dahl,C.R. and Hillman,J.L.
Polypeptides and corresponding molecules for disease detection and
treatment
Patent: WO 0162922-A 12 30-AUG-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
1. .2110
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Incyte ID No: LG:247384.1:2000MAY19"

ORIGIN

Query Match 46.8%; Score 747.8; DB 6; Length 2110;
Best Local Similarity 82.8%; Pred. No. 2.7e-163;
Matches 854; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 262 GACGACAGTGGGCAAGACAGTGCATTTCAAAGCAATATGGATTATAATATAGCTGAT 321
DB |||||
QY 322 TCCTGATGANNAGCTATGGAGNACCTGGAGAGCAGCTGATCGCCCATCTGCTCGA 381
DB |||||
QY 148 CCAGGATGGGAATCCCATGGAGAACTTGAGAGCAGCTGATCGCCCATCTGCTCGA 207
QY 382 GATGTTTACCAAGCCTGTGTCTATCTGCTGCCCTGCCAACCAACCTCTGCCGGAAGTGTC 441
DB |||||
QY 208 GATGTTTACCAAGCAGTGTCTATCTTCGCGTCCAGACCACTGTGCCGGAAGTGTC 267
QY 442 CAACGACATCTTCCAGGCTCGGAATCCCTACTGGAACCAACCGGTGGCTCAGTGTCAT 501
DB |||||
QY 268 CAATGATATTTCCAGGCTCTAACCGTATTGTCGCCCAAGAGGAGGTACCAACATGC 327
QY 502 GTCGAGCTCGTTTCGGTTCGCTCGCCCTCGCGCCATGAAGTATCATGGACCGGACCG 561
DB |||||
QY 328 ATCAGGGGCGGATTCGGTGCCTTCCATGCTGTAGACATGAAGTGGTTTGGATAGACATGG 387
QY 562 GGTGTACGGCTGTCAGAGGAACCTGCTGTGTGGAACCAACATTTGACATCTACAAGCAGA 621
DB |||||
QY 388 GGTATATGACATTCAGAGGAACTGCTGTGTGAGAACATCATCGACATCTACAAACAGA 447
QY 622 GTGCTCAGTGGCCCTCGAGAAAGGACGACCCGATGTGCAAGGAACAGCAAGACGA 681
DB |||||
QY 448 GTGCTCAGTGGCCCTGTCAGAAAGGCGAGTCACCCCATGTGCAAGGAGCAGCAAGATGA 507
QY 682 GAAGATCAACATCTACTGTCTACGNTGAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 741
DB |||||
QY 508 GAAATCAACATCTACTGTCTACGNTGAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 567
QY 742 TGGGGCTCACCAGGCTGTGAGGTTGCCCTTTGCCAAGCATCTTCCAAAGGACAGAAAGAC 801
DB |||||
QY 568 TGGATTCACAGGCTGCGAGGTGCCCCCATTTGACAGTGTCTTCCAGGACAAAGAC 627
QY 802 TGAGCTGAGTAATGATCATCTCAATGTGTGTGGGGGGAACGACCCGAGTGCACAGATCAT 861
DB |||||
QY 628 TGAATGAAATTAATGTATCTCCATGCTGTGGGGGGAATGACCGGTGTGCAGACCATCAT 687
QY 862 CTCTCAGCTGGAGGATCTGTGCAGAGTGCACCAAGGAAATAGCCACGAGTGAAGGAGA 921
DB |||||
QY 688 CACTCAGCTGGAGGATTTCCCGTGCAGTGCACCAAGGAAACAGTCACAGGTAAAGGAGA 747
QY 922 GCTGAGTCAGAAAGTTTGAACCCCTCTACGCCCATCTCTGGAATGAGAAAGAGCGAGTCT 981
DB |||||
QY 748 GCTGAGCCAGAAAGTTTGAACCGTTGTATGCCATCTCTGGATGAGAAAGTGAAGTGTCT 807
QY 982 GCAGCGGATCA GCAGGAGCAGAGAGAAAGCTGGGCTTCATCGAGGCTCTGATCTCTCA 1041
DB |||||
QY 808 GCAGCGGATCA GCAGGAGCAGAGAGAAAGCTTAGCTTTCATCGAGGCGCTCTATCCAGCA 867

QY 1042 GTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACGGCCATCCAGTCCCTGGA 1101
DB |||||
QY 868 GTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAAAAGTCCATCCAGTCCCTGGA 927
DB |||||
QY 1102 TGAGCCCGAGAGGGGTACCTTCTCTCAAGTCCCAAGCAGAGCTCATCAAGAGCATTTAGA 1161
DB |||||
QY 928 CGAGCTGGGGAGCCACCTTCTTGTACTGCCAAGCAACTCATCAAAAGCATTTGGA 987
QY 1162 AGCTTCCAAAGGCTGCCAGCTGGGGAAGACAGAGCAAGGCTTTGAGAAACATGGACTTCT 1221
DB |||||
QY 988 AGCTTCCAAAGGCTGCCAGCTGGGGAAGACAGAGCAGAGGCTTTGAGAAACATGGACTTCT 1047
QY 1222 TACTCTGAGTCTTAGAACATAGCAGAGGCTTTGAGGCGCATTTGAGGACAGGTAA 1281
DB |||||
QY 1048 TACTTTGGATTATAGACACATAGCAGCGCCCTTGAGAGCCATTTGACTTTGGGACAGATGA 1107
QY 1282 AGGATCTGATG 1292
DB |||||
QY 1108 GGAAGAGGAAG 1118

RESULT 15
BX929474 1248 bp mRNA linear VRT 02-FEB-2004
LOCUS
DEFINITION
Gallus gallus finished cDNA, clone CHEST186n9.
ACCESSION
BX929474
VERSION
BX929474.1 GI:41629941
KEYWORDS
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1248)
Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
Croning,M.D.R., Davies,R.M., Francis,M.D., Graham,D.V.,
Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
Tickle,C. and Wilson,S.A.
Direct Submission
Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: chickest@bms.unist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cdna
sequencing project.
This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cdna collection,
from a library constructed by Elizabeth Bosch. cdna was prepared
from RNA extracted from muscle, normalised, and poly A-trimmed.
EcoRI-NotI cut cdna was then ligated into the vector. Vector:
pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia
coli DH10B.
Location/Qualifiers
1. .1248
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST186n9"
/clone_lib="CSEQUEN11"
/dev_stage="adult"

FEATURES
source

ORIGIN

Query Match 38.4%; Score 613.6; DB 5; Length 1248;
Best Local Similarity 76.7%; Pred. No. 4.6e-132;
Matches 764; Conservative 0; Mismatches 229; Indels 3; Gaps 1;

QY 299 ATGGATTATTAATCTAGCTGATTCCTGATGAAACGCTATCGAAGCCTGAGAGCAG 358
DB |||||
QY 28 ATGGATTTCCAGCCAGACATCTCGCGATGCGCCCATCGAGAGCTTGGAGAGCAG 87
DB |||||
QY 359 CTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGCTCATCTCGCTGCCCAA 418
DB |||||

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2005, 08:39:05 ; Search time 299 Seconds
(without alignments)
8739.578 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 1597
Sequence: 1 ctcgagattacccttacag.....gaaataattatctctgtgcc 1597

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1597	100.0	1597	4	US-09-908-988B-5
2	747.8	46.8	1757	3	US-09-484-970B-37
3	484.6	30.3	1431	4	US-09-908-988B-1
4	432.2	27.1	2590	4	US-09-908-988B-3
5	109.8	6.9	4867	4	US-09-949-016-13746
6	86.6	5.4	3262	3	US-09-561-989-9
7	86.6	5.4	3480	4	US-09-799-451-407
8	80.6	5.0	1822	4	US-09-799-451-946
9	73.6	4.6	4843	4	US-09-949-016-15195
10	57.6	3.6	51259	3	US-08-781-891-209
11	57.6	3.6	51259	4	US-09-618-166-209
12	54.6	3.4	2321	4	US-09-949-016-1771
13	54.2	3.4	1071	4	US-09-902-540-8891
14	54.2	3.4	9097	4	US-09-902-540-947
15	53.4	3.3	1960	2	US-08-533-306A-1
16	53.4	3.3	1960	2	US-08-742-923A-1
17	53.4	3.3	2680	2	US-08-533-306A-5
18	53.4	3.3	2680	2	US-08-742-923A-5
19	53.4	3.3	2887	2	US-08-533-306A-3
20	53.4	3.3	2887	2	US-08-742-923A-3
21	53.4	3.3	5574	4	US-09-917-254-40
22	53.4	3.3	6861	4	US-09-949-016-1240
23	53.4	3.3	6861	4	US-09-949-016-1241
24	53.4	3.3	6861	4	US-09-949-016-1242
25	52.8	3.3	601	4	US-09-949-016-61052
26	52.8	3.3	17415	4	US-09-949-016-13513
27	52.4	3.3	9840	3	US-09-534-638-1

c	28	52.2	3.3	1335	4	US-09-774-528-33	Sequence 33, Appl
	29	51.6	3.2	2743	3	US-09-060-482-3	Sequence 3, Appl
	30	50.4	3.2	1588	4	US-09-490-291-7	Sequence 7, Appl
	31	50	3.1	48974	3	US-08-920-422-17	Sequence 17, Appl
	32	50	3.1	90050	3	US-09-245-041-5	Sequence 5, Appl
	33	50	3.1	90050	4	US-08-358-055B-5	Sequence 5, Appl
	34	50	3.1	90050	4	US-08-893-238-5	Sequence 5, Appl
	35	49.8	3.1	2900	4	US-10-087-402-3	Sequence 64, Appl
	36	49.4	3.1	3217	3	US-09-232-200-64	Sequence 64, Appl
	37	49.4	3.1	3217	3	US-09-232-197-64	Sequence 64, Appl
	38	49.4	3.1	3217	3	US-09-232-201-64	Sequence 64, Appl
	39	49.4	3.1	3217	4	US-09-232-195-64	Sequence 5, Appl
	40	49.2	3.1	6644	4	US-08-875-435B-5	Sequence 5, Appl
	41	49.2	3.1	26700	1	US-08-472-217-1	Sequence 1, Appl
	42	49.2	3.1	26700	2	US-08-488-199-5	Sequence 5, Appl
	43	49.2	3.1	26700	3	US-08-760-534A-1	Sequence 1, Appl
	44	49.2	3.1	26700	4	US-09-336-757-1	Sequence 1, Appl
c	45	48.6	3.0	14707	4	US-09-312-762A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-908-988B-5
; Sequence 5, Application US/09908988B
; Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (299)..(1327)
US-09-908-988B-5

Query Match	100.0%	Score	1597;	DB	4;	Length	1597;
Best Local Similarity	100.0%	Pred. No.	0;				
Matches	1597;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	CTCAGAGTTTACCCCTTACAGAACTGTTCCGGAGACCTTTCCCTTGGCAGCACACTCAG	60				
Db	1	CTCAGAGTTTACCCCTTACAGAACTGTTCCGGAGACCTTTCCCTTGGCAGCACACTCAG	60				
Qy	61	GGACGGACGGCAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTTCCAAAGAGCA	120				
Db	61	GGACGGACGGCAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTTCCAAAGAGCA	120				
Qy	121	GCAGACCATGATTAATCTGGGAAAGCAACTGATCTGCCATCTGCTAGAGATTTTAC	180				
Db	121	GCAGACCATGATTAATCTGGGAAAGCAACTGATCTGCCATCTGCTAGAGATTTTAC	180				
Qy	181	GAAGCTGTGTCTTCTCCCTTGCACACAACTGTCAGGAAATGTGGGGCCCCC	240				
Db	181	GAAGCTGTGTCTTCTCCCTTGCACACAACTGTCAGGAAATGTGGGGCCCCC	240				
Qy	241	TTGGAGACAAAGACTTGTGTGACCGAGTGGGCAAGACAGTCGATTTTCAAGCAATAT	300				
Db	241	TTGGAGACAAAGACTTGTGTGACCGAGTGGGCAAGACAGTCGATTTTCAAGCAATAT	300				
Qy	301	GGATTATAATCTAGCTGATTTCTGTGATGGAAACGCTTATGGAGAACCTGGAGAGCAGCT	360				

Db 301 |||||GGATTATAAACTCTAGCGCTGATTCCTGATGGAACCGCTATGGAGAACTCTGGAGAAGCAGCT 360
Qy 361 GATCTGCCCATCTGCTCTGAGATGTTTACCAAGCCTGTGGTCACTCTGCTGCCCTGCCAACA 420
Db 361 GATCTGCCCATCTGCTCTGAGATGTTTACCAAGCCTGTGGTCACTCTGCTGCCCTGCCAACA 420
Qy 421 CAACCTCTGCCGAAGTGTCCCAACGACATCTTCCAGGCTGCCAATCCCTACTGGAACCAA 480
Db 421 CAACCTCTGCCGAAGTGTCCCAACGACATCTTCCAGGCTGCCAATCCCTACTGGAACCAA 480
Qy 481 CCOCGGTGGCTCAGTGTCCATGTCTGAGAGTCCGTTCCGTTGGCCCTCTGTCGCGCCCATGA 540
Db 481 CCOCGGTGGCTCAGTGTCCATGTCTGAGAGTCCGTTCCGTTGGCCCTCTGTCGCGCCCATGA 540
Qy 541 AGTGATCATGGACCGGACCGGGGTGTACGGCCTGCGAGAGAACTCTGCTGGTGGAAAAACAT 600
Db 541 AGTGATCATGGACCGGACCGGGGTGTACGGCCTGCGAGAGAACTCTGCTGGTGGAAAAACAT 600
Qy 601 CATTGACATCTACAGCAGGAGTCTCCAGTCCGCCCTCGCAGAAAGGCGACCCCGAT 660
Db 601 CATTGACATCTACAGCAGGAGTCTCCAGTCCGCCCTCGCAGAAAGGCGACCCCGAT 660
Qy 661 GTGCAAGGAACACGAAGACGAGAATCAACATCTACTGTCTCACGTGTGAGGTGCTTAC 720
Db 661 GTGCAAGGAACACGAAGACGAGAATCAACATCTACTGTCTCACGTGTGAGGTGCTTAC 720
Qy 721 TTGCTCTCTGTGCAAGTGTCTGGGGCTCACAGGGCTGTGAGGTGCGCCCTTTGCAAG 780
Db 721 TTGCTCTCTGTGCAAGTGTCTGGGGCTCACAGGGCTGTGAGGTGCGCCCTTTGCAAG 780
Qy 781 CATCTTCCAGGACAGAACTCAGCTGAGTAACTGATCTCATCTGCTGCTGGTGGCGGAA 840
Db 781 CATCTTCCAGGACAGAACTCAGCTGAGTAACTGATCTCATCTGCTGCTGGTGGCGGAA 840
Qy 841 CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTGCTGCAGAGTGACCAAGGAGAA 900
Db 841 CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTGCTGCAGAGTGACCAAGGAGAA 900
Qy 901 TAGCCACAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGAACCCCTCTACGCCATCTCTGA 960
Db 901 TAGCCACAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGAACCCCTCTACGCCATCTCTGA 960
Qy 961 TGAGAAGAGAGCGAGCTGCTGAGCGGATCAAGCAGGAGCAGGAGAGAGCTGGGCTT 1020
Db 961 TGAGAAGAGAGCGAGCTGCTGAGCGGATCAAGCAGGAGCAGGAGAGAGCTGGGCTT 1020
Qy 1021 CATCGAGCTCTGATCTCCAGTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTGA 1080
Db 1021 CATCGAGCTCTGATCTCCAGTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTGA 1080
Qy 1081 GACCGCATCCAGTCTGATGAGCCCGGAGGGCTACCTTCTCTCAAGTCCCAAGCA 1140
Db 1081 GACCGCATCCAGTCTGATGAGCCCGGAGGGCTACCTTCTCTCAAGTCCCAAGCA 1140
Qy 1141 GCTCATCAAGAGCATTTGTAAGCTTCCAAAGGCTGCGAGTGGGAGAGAGAGGCAAGG 1200
Db 1141 GCTCATCAAGAGCATTTGTAAGCTTCCAAAGGCTGCGAGTGGGAGAGAGAGGCAAGG 1200
Qy 1201 CTTTGAGAACATGGAATCTTTTACTCTGGAATTAGAACATAGCAGAGCCCTTGAGGGC 1260
Db 1201 CTTTGAGAACATGGAATCTTTTACTCTGGAATTAGAACATAGCAGAGCCCTTGAGGGC 1260
Qy 1261 CATTGACTTTGGACAGGTAAAGATGTGATGTTTCACTGTTGACCTTTGAAGGAGCGG 1320
Db 1261 CATTGACTTTGGACAGGTAAAGATGTGATGTTTCACTGTTGACCTTTGAAGGAGCGG 1320
Qy 1321 TTCTCTTTGAGTTCTGAGGGAACTGTAAAGGCTCAAAATTTACACAGCCAGTGTGAC 1380
Db 1321 TTCTCTTTGAGTTCTGAGGGAACTGTAAAGGCTCAAAATTTACACAGCCAGTGTGAC 1380
Qy 1381 AGTCTCTCTATGGAGCCCTGATGTTTGTAGTGTCTTAAGTGTAGACCAAGCTGCTGG 1440

Db 1381 AGTCTCTCTATGAGCCCTGACTGCTTTAGTAGTGTCTAAAGTAGACCAAGCTGGTCTGG 1440
Qy 1441 AACACATAGAGATCTATCTTGGCCATCTCTGCTTCTTGGGGATGAGATAAAGGCATGT 1500
Db 1441 AACACATAGAGATCTATCTTGGCCATCTCTGCTTCTTGGGGATGAGATAAAGGCATGT 1500
Qy 1501 GOCACCATGCTGGCTCCACAGACAACTTGTGTAGTGAATCCAGGCTCTGGGCACAGTGCC 1560
Db 1501 GOCACCATGCTGGCTCCACAGACAACTTGTGTAGTGAATCCAGGCTCTGGGCACAGTGCC 1560
Qy 1561 TGGTACATAAATGTTTCGAAATAAATTAATCTCGTGCC 1597
Db 1561 TGGTACATAAATGTTTCGAAATAAATTAATCTCGTGCC 1597

RESULT 2
US-09-484-970B-37
; Sequence 37, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmoth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 37
; LENGTH: 1757
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 247384.1CB1
US-09-484-970B-37

Query Match 46.8%; Score 747.8; DB 3; Length 1757;
Best Local Similarity 82.8%; Pred. No. 6.4e-205;
Matches 854; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 262 GACGAGGTGGGCAAGACAGATCGCATTTCAAAGCAATATGGATTATAAAATCTAGCCTGAT 321
Db 88 GAGGAGCTAGGGTGGCTCTCATTTCCCAAGATGGATTATAAGTCGAGCCTGAT 147
Qy 322 TCCTGATGAAACGGTATGGAGAACTGGAGAGAGAGCTGATCTGCCCATCTGCCCTGGA 381
Db 148 CCAGGATGGGAATCCCATGGAGAACTTGGAGAGAGAGCTGATCTGCCCTATCTGCCCTGGA 207
Qy 382 GATGTTTACCAAGCCCTGTGCTCATCTGCCCTGCCAACAACCTCTGCCGGAAGTGTC 441
Db 208 GATGTTTACCAAGCCAGTGGTCACTTTCGCTGCCAGCAACCTCTGCCGGAAGTGTC 267
Qy 442 CAACGACATCTTCCAGGCTCGGAATCCCTACTCGACCAACCCGGTGGCTCAGTGTCCAT 501
Db 268 CAATGATATTTCCAGGCTCTTAAACCGTATTTGCCCAAGAGGAGGTACCAACCATGGC 327
Qy 502 GTCTGAGAGTGTGTTCCGTTGGCCCTCTGTCGCCGCATGAAGTGAATCATGGACCGGACGG 561
Db 328 ATCAGGGGCGCATTCCTGCTGCCCATCTCTGTAGACATGAAGTGGTTTGGTAGACATGG 387
Qy 562 GGTGTACGCGCTGCAGAGGAACCTGCTGTTGAAACATCATTTGACATCTTACAAGCAGGA 621
Db 388 GGTATATGACATTCAGAGGNACTGCTGTTGGAGAAACATCATCGACATCTTACAACAGGA 447
Qy 622 GTGCTCCAGTCGGCCCTCTGCAGAAAGGAGCCACCCGATGTGCAGAGGAACAACGAGACGA 681
Db 448 GTGCTCCAGTCGGCCCTCTGCAGAAAGGAGGTACACCCCATGTGCAGAGGAGCAACGAGATGA 507
Qy 682 GAAAGTCAACATCTACTGTCTCAGTGTGAGGTGCTTCTGCTCTGTTGCAAGTGT 741
Db 508 GAAATCAACATCTACTGTCTCAGTGTGAGGTGCTTCTGCTCTGTTGCAAGTGT 567

QY 742 TGGGGCTCACCAGGCTGTAGTTGGCCCTTTGCAAGCATTTTCCAAAGGACAGAAC 801
DB 568 TGGGATCCACAAGGCTGCGAGGTGGCCCAATTCAGAGTGTCTTCCAGGGACAAAAGAC 627
QY 802 TGAGCTGAGTACTCANTCTCCTGCTGGTGGGGGGAACCGAGTGCAGACCATCAT 861
DB 628 TGAATCGAATAACTGTATCTCCATGCTGGTGGGGGAATGACCGGTGCAGACCATCAT 687
QY 862 CTCTCAGCTGGAGGACTCGTGAGAGTGAACCAAGAGAGATAGCCACAGGTGAAGAGGA 921
DB 688 CACTCAGCTGGAGGATCTCCGTCGAGTGAACCAAGAGAGACAGTCAACAGGTAAAGAGA 747
QY 922 GCTGAGTCAGAGTTTGACACCTCTACGCCATCTGAGATGAGAGAGAGAGCTGCT 981
DB 748 GCTGAGCCAGAGTTTGACACCTCTGATGATGATGATGATGATGATGATGATGATGAT 807
QY 982 GCAGCGGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1041
DB 808 GCAGCGGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 867
QY 1042 GTACAGGAGGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1101
DB 868 GTACAGGAGGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 927
QY 1102 TGAGCCCGAGGGGTACTCTCTCAAGTCCCAAGCAGGCTCATCAAGAGCATTTGTAGA 1161
DB 928 CGAGGCTGGGGGAGCCACCTCTCTGACTGCCAAGCAACTCATCAAAAGCATTTGTGA 987
QY 1162 AGCCTCCAGGGCTCCAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1221
DB 988 AGCTTCCAGGGCTCCAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1047
QY 1222 TACTCTGAGTTAGAACACATAGCAGAGGCTTGAGGGCATTGACTTTGGGACAGGTAA 1281
DB 1048 TACTTTGGATTAGGACATAGCAGAGGCTTGAGGGCATTGACTTTGGGACAGGTAA 1107
QY 1282 AGGATGTGATG 1292
DB 1108 GGAAGAGGAAG 1118

RESULT 3
US-09-908-988B-1
; Sequence 1, Application US/09908988B
; Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028US
; CURRENT FILING DATE: 2000-07-18
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1296)
US-09-908-988B-1

Query Match 30.3%; Score 484.6; DB 4; Length 1431;
Best Local Similarity 69.2%; Pred. No. 4.2e-129;
Matches 677; Conservative 0; Mismatches 299; Indels 3; Gaps 1;
QY 317 CTGATTCTGTGAGAAACCTTATGGAGAACCTTGGAGAACCTTATCTGCCCCCATCTGCG 376
|||||

DB 226 CTGCTAGGGATGCGCAACAACATGGAACAATTGGAGAGAGCTCATTTTGGCCCCATCTGC 285
QY 377 CTGGAGATGTTTACCAAGCCTGTGTCTATCTCTGCCCTGCCCAACAACAACCTCTTGC CGGAG 436
DB 286 CTGGAGATGTTTCTCAAGCCGCTGTGTGTATCTTGGCCCTGCCAACAACAACCTGTGCGCAG 345
QY 437 TGTGCAACGACATCTTCCAGGCTGCGAATCCCTACTTGGAACAACCGCGGTGGCTCAGTG 496
DB 346 TGTGCAACGACGCTTCTCCAGGCTCTAATCTCTGTGGCAATCCCGGGGCTCCCAACG 405
QY 497 TCCATGCTCGAGGTGCTTCCGTTGGCCCTCTGTCGCCCATGAAGTGAATCATATGACACCG 556
DB 406 GTGTCTTCAGAGGAGGCTTCCGATGCCCATCTTGTAGGACGAGGTGTCTCTGACAGG 465
QY 557 CACGGGTGTACGGCTGCAGAGGAACCTGTGTGGGAAACATCATTTGACATCTTACAG 616
DB 466 CATGTGTCTATGGCTCGACGGAACTGTCTAGTGGAGAACATCATTTGACATCTTACAG 525
QY 617 CAGGATGCTCAG---TCGGCCCTGCAGAAAGCAGCACCCTGATGTGCNAGGAACAC 673
DB 526 CAGGATGCTCCTCCGGCCACTGCAGCCAAAGCTGAACAGCACCTCATTTGTGAGAGCAC 585
QY 674 GAAGACGAGAAAGATCAACATCTACTGTCTCACTGTGAGGTGCTTACTTGTCTCTTGTGC 733
DB 586 GAGGACGAGAAAGATCAACATCTACTGTCTGAGTGTGAGGTGCTTACTTGTCTCTTGTGC 645
QY 734 AAGGTGTTGGGGCTCACAGGCTGTGAGGTGCTTGTGCAAGAGCATTTTCAAGAGA 793
DB 646 AAGGTGTTGGGGCTCACAGGCTGTGAGGTGCTTGTGCAAGAGCATTTTCAAGAGA 705
QY 794 CAGAAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 853
DB 706 CAGAAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 765
QY 854 ACGATCATCTCTCAGCTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 913
DB 766 GAGTGTATACCCAGATGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 825
QY 914 AAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 973
DB 826 AAGCAACTGTTAAACCAAGAGTTCGAGACCTCTGTGCGCGTTCGAGAGCGGCAAGGCG 885
QY 974 GAGTGTGTGAGCGGATCACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1033
DB 886 GAACTGTCTTCAAGCAGTGTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 945
QY 1034 ATCTCTCAGTACAGGAGCAGCTGGAAGTCCCAAGTGTGAGAGCCGCAACCTTCCAG 1093
DB 946 ATCCGCGAGTACGAGAGCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1005
QY 1094 TCCCTGAGTACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
DB 1006 TCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1065
QY 1154 ATTGTAGAGGCTTCAAGGCTGCCAGTGGGAGAGAGAGAGAGAGGCTTTGAGAACATG 1213
DB 1066 CTCGGGGCAATGTCGAGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1125
QY 1214 GACTACTTTTACTCTGAGTGTAGAACACATAGCAGAGGCTTTGAGGGCCATTCACATTTGG 1273
DB 1126 GAGCAATTTCTCTGTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1185
QY 1274 ACAGGTAAGGATGTGATG 1292
DB 1186 CCGGGCGCGCTGGGGATG 1204

RESULT 4
US-09-908-988B-3
; Sequence 3, Application US/09908988B
; Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC

APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
FILE REFERENCE: MYOG:028US
CURRENT APPLICATION NUMBER: US/09/908,988B
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,020
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 2590
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (80)..(1714)
US-09-908-988B-3

Query Match 27.1%; Score 432.2; DB 4; Length 2590;
Best Local Similarity 66.5%; Pred. No. 7.5e-114;
Matches 636; Conservative 0; Mismatches 318; Indels 3; Gaps 1;

QY 336 CTATGGAGAACTGGAGAACAGCTGATCTGCCCCATCTCCCTGGAGATGTTTACCAAGC 395
DB 126 CCATGGATAACTTGGAAAGCAACTGATCTGTCCATCTGCCTAGAGATGTTTCAAGAAC 185
QY 396 CTGTGGTCATCTGCCCCCTCCACACACAACTCTGCCGGAAGTGTGCCAAGACATCTTCC 455
DB 186 CTGTGGTCATCTGCCCCCTGCCAGACAACTGTGCAGAAATGTGCCAGTGACATCTTCC 245
QY 456 AGGTGCGAATCCCTACTGTGACCAACCGCGTGGCTCAGTGTCCATGTCTGGAGGTGCTT 515
DB 246 AGGCTCTAACCGTACTTACCCACACAGAGAGGACCAACCGTGGCATCAGGGGGCGCT 305
QY 516 TCGTGTGCCCCCTCGTCCGCCATGAAGTGAATCATGTACATCTTACAGCAGGAGTGTCCAGTCCGC 635
DB 366 AGAGGAACCTGCTCGTGGAAACATTTATGATATCTACAGCAGGAATCCACCA---GGC 422
QY 636 CCCTGCAAGAAAGGAGCAGCCCGATGTGCAAGGAACACGAGAACGAGATCAACATCT 695
DB 423 CAGAAAAAATTGGACCCAGCCATGTGTGAAGAGCATGAAGAGAACGATCAACATCT 482
QY 696 ACTGTCTCAGTGTAGGTGCTTACTGTCTCTTGTGCAAGGTGTTTGGGGCTCAACAG 755
DB 483 ATTGTCTGAACCTGTGAAGTGTCCCACTGTCTTGTGCAAGGTGTTTGGGGCTCAACAG 542
QY 756 CTTGTGAGGTGCTCCCTTTTCCAAAGCATCTTCCAGGACAGAGATCTGAGCTGAGTAAT 815
DB 543 ACTGCCAGGTGGCTCCCTTACTCATGTGTGTCCAGAGGCGAAGTCCAGTCTCAGTGATG 602
QY 816 GCATCTCCATGCTGTGGGGGGAACGACCGAGTGCAGACGATCATCTCTCAGCTGGAGG 875
DB 603 GTATTGTGTACTTGTGGGAAGCAACGATAGATCCAGGGTGTGATCAGCCAGCTGGAGG 662
QY 876 ACTGTGTCAGAGTGACCAAGAGAGATAGCCACGAGTGAAGGAGGAGCTGAGTCAGAAAT 935
DB 663 ACACCTGTAAAACTATTGAGGAGTGTCTGCAAGAAAGCAGAAACAGGACCTGTGTGAGAAAT 722
QY 936 TTCACACCTCTAGCCATCTCGATGATGAGAGAGAGCGAGTGTGTCAGCGGATCAAGC 995
DB 723 TTGATACCTTATAGGATCTCTGAGAGAGGAGAACTGAAATGACCCAGGCCATCACTC 782
QY 996 AGGAGCAGGAGGAGAGCTGGGCTTTCATCCAGGCTCTGATCTCCAGTACAGGAGCAGC 1055
DB 783 GAACACAGGAGGAGAACTGGAACATCTCCGACTCTTATCAGGAAGTATTCGATCACC 842
QY 1056 TGGAAAGTCCCAAGCTGTGTGGAGACCGCCATCCAGTCCCTGGATGAGCCCGGAGGGG 1115

DB 843 TGGAGAACTGATCCAAAGTTGGTGGAGTCAGGAATCCAGTTCTGATGAGCCGCAATGG 902
QY 1116 CTACCTTCTCTCAAGTGCACAGCAGCTCATCAAGAGCATTTGTAGAGCCTTCAAGGGCT 1175
DB 903 CAGTATTTCTGCAGAAATGCCAAGCCCTGTTGCAAAAGATCGTGAAGCATCAAGAGCGT 962
QY 1176 GCCAGCTGGGAAGACAGACGAGGCTTTGAGAAACATGAGTACTTACTCTTGGACTTAG 1235
DB 963 TTCAGATGAGAAACTAGAACAGGTTATGAGATCATGAGCAACTTCACTGTCAATCTCA 1022
QY 1236 AACACATAGCAGAGCGCTTTGAGGGCCATTTGAGGACAGGTAAGGATGTGATG 1292
DB 1023 ATAGAGAGAAAAAATATATCCGTGAAATTCAGCTTTCTAGAGAAAGGAGGAGAG 1079

RESULT 5
US-09-949-016-13746/c
Sequence 13746, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13746
LENGTH: 4867
TYPE: DNA
ORGANISM: Human
US-09-949-016-13746

Query Match 6.9%; Score 109.8; DB 4; Length 4867;
Best Local Similarity 67.0%; Pred. No. 9.3e-21;
Matches 156; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 894 AGGAGAAATAGCCACCAAGTGAAGGAGGAGCTGAGTCAGAGATTGACACCCCTACGCCA 953
DB 4681 AGCAATAGCCGAGGAGGAGGAGGAGTGTGTTAAACAGAGGTTTGAGAGCTGTGCGCAG 4622
QY 954 TCTGTGATGAGAAAGAGAGCGAGCTGCTGAGCGGATCACGAGGAGCAGGAGGAGAAGC 1013
DB 4621 TGTGAGGAGCGCAGGAGGAGGAGTGTGCTGAGCGCTGGCCCGGAGCAAGAGGAGAAGC 4562
QY 1014 TGGCTTTCATCAGGCTGTGATCTCCAGTACAGGAGCAGCTGGAAGAAAGTCCACCAGC 1073
DB 4561 TGCAGGCGCTGCGCGGCTCATCCGTCAGTATGGCGACCACTTGGAGGCTCTCTTAAGC 4502
QY 1074 TTGTGAGACCGCATCCAGTCCCTGAGTGAGCCGAGGGGCTACTTCTCTC 1126
DB 4501 TGTGAGAGTGTGCTCATCCAGTCCATGGAAGAGCCACAAATGGCGCTGTATCTC 4449

RESULT 6
US-09-561-989-9
Sequence 9, Application US/09561989
Patent No. 6468750
GENERAL INFORMATION:
APPLICANT: KOLLER, Klaus-Peter
TITLE OF INVENTION: No. 6468750e1 Cell Regulation Factor T7020
FILE REFERENCE: seq
CURRENT APPLICATION NUMBER: US/09/561,989
CURRENT FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2005, 11:08:50 ; Search time 918 Seconds
(without alignments)
10784.204 Million cell updates/sec

Title: US-10-775-649-5

Perfect score: 1597
Sequence: 1 ctcgagattacccttacg.....gaaataaattctcgtgcc 1597

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*

24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1597	100.0	1597	9	US-09-908-988B-5 Sequence 5, Appli
2	1597	100.0	1597	19	US-10-775-649-5 Sequence 5, Appli
3	1597	100.0	1597	15	US-10-775-627-5 Sequence 20, Appli
4	890.8	55.8	1053	15	US-10-061-043A-20 Sequence 20, Appli
5	890.8	55.8	1053	17	US-10-060-634C-20 Sequence 20, Appli
6	803.8	50.3	2097	15	US-10-061-043A-22 Sequence 22, Appli
7	803.8	50.3	2097	17	US-10-060-634C-22 Sequence 22, Appli

8	802.2	50.2	1764	18	US-10-221-625-192	Sequence 192, App
9	802.2	50.2	2700	20	US-10-723-860-7801	Sequence 7801, Ap
10	800.6	50.1	1764	17	US-10-094-749-1222	Sequence 1222, Ap
11	797.4	49.9	1781	9	US-09-764-864-21	Sequence 21, Appl
12	747.8	46.8	2110	21	US-10-204-921-12	Sequence 12, Appl
13	547.4	34.3	630	15	US-10-061-043A-32	Sequence 32, Appl
14	547.4	34.3	630	17	US-10-060-634C-32	Sequence 32, Appl
15	484.6	30.3	1431	9	US-09-908-988B-1	Sequence 1, Appli
16	484.6	30.3	1431	19	US-10-775-649-1	Sequence 1, Appli
17	484.6	30.3	1431	19	US-10-775-627-1	Sequence 1, Appli
18	481.8	30.2	1913	10	US-09-890-688-57	Sequence 57, Appl
19	444.4	27.8	867	15	US-10-061-043A-38	Sequence 38, Appl
20	444.4	27.8	867	17	US-10-060-634C-38	Sequence 38, Appl
21	432.2	27.1	2590	9	US-09-908-988B-3	Sequence 3, Appli
22	432.2	27.1	2590	19	US-10-775-649-3	Sequence 3, Appli
23	432.2	27.1	2590	19	US-10-775-627-3	Sequence 3, Appli
24	430.6	27.0	1925	17	US-10-104-047-673	Sequence 673, App
25	430.6	27.0	2434	19	US-10-473-574-36	Sequence 36, Appl
26	430.6	27.0	2634	17	US-10-104-047-433	Sequence 433, App
27	430.6	27.0	2662	20	US-10-723-860-7135	Sequence 7135, Ap
28	421.2	26.4	1762	9	US-09-764-864-34	Sequence 34, Appl
29	390	24.4	531	11	US-09-864-408A-6101	Sequence 6101, Ap
30	329.4	20.6	2040	18	US-10-250-613-22	Sequence 22, Appl
31	277	17.3	1039	9	US-09-880-192-25	Sequence 25, Appl
32	277	17.3	1039	16	US-10-427-348-25	Sequence 25, Appl
33	260.6	16.3	424	10	US-09-918-995-5316	Sequence 5316, Ap
34	246.4	15.4	411	10	US-09-918-995-4809	Sequence 4809, Ap
35	244.2	15.3	446	9	US-09-764-864-482	Sequence 482, App
36	217.8	13.6	587	9	US-09-764-864-493	Sequence 493, App
c 37	156.8	9.8	638	17	US-10-191-803-895	Sequence 895, App
38	141.6	8.9	766	20	US-10-723-860-7957	Sequence 7957, Ap
c 39	141.6	8.9	2000	14	US-10-198-846-10290	Sequence 10290, A
40	123.4	7.7	475	20	US-10-723-860-4075	Sequence 4075, Ap
41	101.4	6.3	3127	17	US-10-108-260A-1109	Sequence 1109, Ap
42	100.2	6.3	498	10	US-09-918-995-32020	Sequence 32020, A
43	87.4	5.5	728	20	US-10-425-115-83161	Sequence 83161, A
44	86.6	5.4	3262	14	US-10-237-790-9	Sequence 9, Appli
45	86.6	5.4	3480	18	US-10-302-172-407	Sequence 407, App

ALIGNMENTS

RESULT 1

US-09-908-988B-5
; Sequence 5, Application US/09908988B
; Patent No. US20020127690A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (299)..(1327)
US-09-908-988B-5

Query Match 100.0%; Score 1597; DB 9; Length 1597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGAGATTACCTTACAGAGCTGTCGGAGCACCTTCCTCCCTGGCAGCACACTCAG 60

Db 1 |||||CTCGAGATTATCCCTTACAGAAGCTGTTCGGAGCACCTTTCTCCTTGGCAGCACACTCAG 60
Qy 61 GGNACGGGACGGCAAGGAATGAGCACTTCTCTGAATTACAAGTCTTTTCTCCTCAAGAGCA 120
Db 61 GGNACGGGACGGCAAGGAATGAGCACTTCTCTGAATTACAAGTCTTTTCTCCTCAAGAGCA 120
Qy 121 GCAGACCATGAGTAACTTGGAAAGCAACTGTCTGTCCCATCTGCTCCTAGAGAGTTTAC 180
Db 121 GCAGACCATGAGTAACTTGGAAAGCAACTGTCTGTCCCATCTGCTCCTAGAGAGTTTAC 180
Qy 181 GAAGCCTGTGTCAATTCTCCCTTGCAGCACAACCTGTGCAGGAATGTGCGGGCCCCC 240
Db 181 GAAGCCTGTGTCAATTCTCCCTTGCAGCACAACCTGTGCAGGAATGTGCGGGCCCCC 240
Qy 241 TTGGAGACAAAGACTTGGTGTGACGAGGTGGGCAAGACAGTCGCAATTTCAAGCAATAT 300
Db 241 TTGGAGACAAAGACTTGGTGTGACGAGGTGGGCAAGACAGTCGCAATTTCAAGCAATAT 300
Qy 301 GGATTATAAATCTAGCTGATTCCTGATGGAAAGCTGTATGGAAACCTGGAGAGCAGCT 360
Db 301 GGATTATAAATCTAGCTGATTCCTGATGGAAAGCTGTATGGAAACCTGGAGAGCAGCT 360
Qy 361 GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTGTCATCTGCTGCCCTGCCAACA 420
Db 361 GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCTGTGTGTCATCTGCTGCCCTGCCAACA 420
Qy 421 CAACCTCTGCCGAAGTGTGCCAAGACATCTTCCAGGCTGCGAATCCCTACTGGACCAA 480
Db 421 CAACCTCTGCCGAAGTGTGCCAAGACATCTTCCAGGCTGCGAATCCCTACTGGACCAA 480
Qy 481 CCGCGTGGCTCAGTGTCAATGCTCGAGGTGCTTTCCGTTGGCCCTCGTGGCCCATGA 540
Db 481 CCGCGTGGCTCAGTGTCAATGCTCGAGGTGCTTTCCGTTGGCCCTCGTGGCCCATGA 540
Qy 541 AGTGATCATGGAACGGGAGTGTACCGGCTGACAGAGAACTCTGCTGGTGGAAAAAT 600
Db 541 AGTGATCATGGAACGGGAGTGTACCGGCTGACAGAGAACTCTGCTGGTGGAAAAAT 600
Qy 601 CATTGACATCTAAGCAGGAGTGTCCAGTGGCCCTGCAAGAGGAGGAGCCAGCT 660
Db 601 CATTGACATCTAAGCAGGAGTGTCCAGTGGCCCTGCAAGAGGAGGAGCCAGCT 660
Qy 661 GTCAAGGAAACAGAGAGAGTCAACATCTACTGTCTCACTGTGTGAGTGTGCTTAC 720
Db 661 GTCAAGGAAACAGAGAGAGTCAACATCTACTGTCTCACTGTGTGAGTGTGCTTAC 720
Qy 721 TTGCTCCTTGTGCAAGTGTGTGGGCTCACAGGCTGTGAGGTGTGCGCCCTTTGCAAG 780
Db 721 TTGCTCCTTGTGCAAGTGTGTGGGCTCACAGGCTGTGAGGTGTGCGCCCTTTGCAAG 780
Qy 781 CATCTTCAAGGACAGAGACTGAGTGAATCTGATCTCCATCTCCATCTGCTGGTGGGGAA 840
Db 781 CATCTTCAAGGACAGAGACTGAGTGAATCTGATCTCCATCTCCATCTGCTGGTGGGGAA 840
Qy 841 CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTGTGCGAGAGTGACCAAGAGAA 900
Db 841 CGACCGAGTGCAGACGATCATCTCTCAGCTGGAGGACTGTGCGAGAGTGACCAAGAGAA 900
Qy 901 TAGCCACCAAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGAACCCCTCTACGCCCATCTCGA 960
Db 901 TAGCCACCAAGGTGAAGGAGAGCTGAGTCAGAAAGTTTGAACCCCTCTACGCCCATCTCGA 960
Qy 961 TGAGAGAGAGGAGCTGCTGAGCGGATCAGCAGGAGCAGGAGGAGAGCTGGCTT 1020
Db 961 TGAGAGAGAGGAGCTGCTGAGCGGATCAGCAGGAGCAGGAGGAGAGCTGGGCTT 1020
Qy 1021 CATCGAGGCTCTGATCTCTCAGTACAGGAGAGCTGGAAGTCCCAAGCTTGTGA 1080
Db 1021 CATCGAGGCTCTGATCTCTCAGTACAGGAGAGCTGGAAGTCCCAAGCTTGTGA 1080
Qy 1081 GACCGCATCTCAGTCTCGATGAGCCCGAGGGGCTACTTCTCTCAAGTGCACAGCA 1140

Db 1081 GACCGCATCTCAGTCTCGATGAGCCCGAGGGGCTACTTCTCTCAAGTGCACAGCA 1140
Qy 1141 GCTCATCAAGAGCATTTAGAGCCCTCCAAGGCTGCCAGCTGGGGAACACAGAGCAAG 1200
Db 1141 GCTCATCAAGAGCATTTAGAGCCCTCCAAGGCTGCCAGCTGGGGAACACAGAGCAAG 1200
Qy 1201 CTTTGAGAACTGGGACTACTTTACTCTGGACTTGAACAACATAGCAGAGGCCCTTGAGGGC 1260
Db 1201 CTTTGAGAACTGGGACTACTTTACTCTGGACTTGAACAACATAGCAGAGGCCCTTGAGGGC 1260
Qy 1261 CATTTGAGCTTTGGGACAGGTAAAGATGTGATGTTTGAATTTTGAAGGAGCG 1320
Db 1261 CATTTGAGCTTTGGGACAGGTAAAGATGTGATGTTTGAATTTTGAAGGAGCG 1320
Qy 1321 TTCTCTTTCAGTCTCGAGGGAACTGTTAAAGAGTCAAAATTTACACGCCAGTGTGAC 1380
Db 1321 TTCTCTTTCAGTCTCGAGGGAACTGTTAAAGAGTCAAAATTTACACGCCAGTGTGAC 1380
Qy 1381 AGGTCTCTCTATGGAGCCCTGACTGTCTTAGTAGTGTCTAAAGTAGACCAAGCTGTCTGG 1440
Db 1381 AGGTCTCTCTATGGAGCCCTGACTGTCTTAGTAGTGTCTAAAGTAGACCAAGCTGTCTGG 1440
Qy 1441 AACACATAGAGATCTATCTTTGCCCATCTCTGCTTTAGGGATGAGATAAAGGATGT 1500
Db 1441 AACACATAGAGATCTATCTTTGCCCATCTCTGCTTTAGGGATGAGATAAAGGATGT 1500
Qy 1501 GCCCACCATGCTGCTGCCACAGACAACTTTGTGATGATCCAGGCTCTGGCACAGTGC 1560
Db 1501 GCCCACCATGCTGCTGCCACAGACAACTTTGTGATGATCCAGGCTCTGGCACAGTGC 1560
Qy 1561 TGGTACATAAATTTGTTTTCGAAATAAATTTATCTCGTGCC 1597
Db 1561 TGGTACATAAATTTGTTTTCGAAATAAATTTATCTCGTGCC 1597

RESULT 2

US-10-775-649-5
; Sequence 5, Application US/10775649
; Publication No. US20040132160A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028USD2
; CURRENT APPLICATION NUMBER: US/10/775,649
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (299)..(1327)
US-10-775-649-5

Query Match 100.0%; Score 1597; DB 19; Length 1597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCGAGATTACCTTACAGAACTGTTCGGAGCACCTTTCCCTTGGCAGCACACTCAG 60
Db 1 CTCGAGATTACCTTACAGAACTGTTCGGAGCACCTTTCCCTTGGCAGCACACTCAG 60
Qy 61 GCACAGGAGCGCAAGGAATGAGCACTTCTGTAATTAAGTCTTTCTCCAAAGCA 120
Db 61 GCACAGGAGCGCAAGGAATGAGCACTTCTGTAATTAAGTCTTTCTCCAAAGCA 120

QY 121 GCAGACCATGGATAACTTGGAAAAAGCAACTGATCTGTCTCCATCTGCCTAGAGATGTTTAC 180
DB 121 GCAGACCATGGATAACTTGGAAAAAGCAACTGATCTGTCTCCATCTGCCTAGAGATGTTTAC 180
QY 181 GAAGCCTGTGCTCATCTCTCCCTTGCAGACACCACTGTGCGAGGAATGTGGGGCCCCC 240
DB 181 GAAGCCTGTGCTCATCTCTCCCTTGCAGACCACTGTGCGAGGAATGTGGGGCCCCC 240
QY 241 TTGGAGACAAGACATCTGTGTGACCGCAGGTGGCAAGACAGTCGATTTCAAAGCAATAT 300
DB 241 TTGGAGACAAGACATCTGTGTGACCGCAGGTGGCAAGACAGTCGATTTCAAAGCAATAT 300
QY 301 GGATTTAAATCTAGCCTGATTTCTGTATGGAAAAAGCTATGAGAAACCTGGAGAACGCT 360
DB 301 GGATTTAAATCTAGCCTGATTTCTGTATGGAAAAAGCTATGAGAAACCTGGAGAACGCT 360
QY 361 GATCTGCCCATCTGCCTGGAGATGTTTACCAAGCCTGTGTCATCTGCCCTGCCACCA 420
DB 361 GATCTGCCCATCTGCCTGGAGATGTTTACCAAGCCTGTGTCATCTGCCCTGCCACCA 420
QY 421 CAACCTCTGCCGGAAGTGTGCCAAGACATCTTCCAGGCTGCGAATCCCTACTGGACCAA 480
DB 421 CAACCTCTGCCGGAAGTGTGCCAAGACATCTTCCAGGCTGCGAATCCCTACTGGACCAA 480
QY 481 CCGGGTGGCTCAGTGTCCATGTCTGGAGGTGTTTCCGTTGCGCTTCCGCTGCCCAATGA 540
DB 481 CCGGGTGGCTCAGTGTCCATGTCTGGAGGTGTTTCCGTTGCGCTTCCGCTGCCCAATGA 540
QY 541 AGTGATCATGCAACCGGCAAGGGGTGTACGGCTGCGAGGAACTGCTGTGGAAAAAT 600
DB 541 AGTGATCATGCAACCGGCAAGGGGTGTACGGCTGCGAGGAACTGCTGTGGAAAAAT 600
QY 601 CATTCACATCTACAGCAGGAGTGTCTCAGTCCGCTCGGCAAGAGGAGGAGGAGGAGGAG 660
DB 601 CATTCACATCTACAGCAGGAGTGTCTCAGTCCGCTCGGCAAGAGGAGGAGGAGGAGGAG 660
QY 661 GTGCAAGGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 661 GTGCAAGGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 TTGCTCTTGTGCAAGGTGTTGGGGCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 721 TTGCTCTTGTGCAAGGTGTTGGGGCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 CATCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 CATCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 CGACGAGTGCAGACGATCATCTCTCAGCTGGAGGAGTCTGTCAGAGTGACCAAGGAGAA 900
DB 841 CGACGAGTGCAGACGATCATCTCTCAGCTGGAGGAGTCTGTCAGAGTGACCAAGGAGAA 900
QY 901 TAGCCACAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 901 TAGCCACAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 TGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
DB 961 TGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 1021 CATCGAGGCTCTGATCTCTCCAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
DB 1021 CATCGAGGCTCTGATCTCTCCAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1081 GACCCGCATCCAGTCTCCAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 GACCCGCATCCAGTCTCCAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GCTCATCAAGACATTTGTAGAGGCTTCCAAAGGCTGCGAGGAGGAGGAGGAGGAGGAGG 1200
DB 1141 GCTCATCAAGACATTTGTAGAGGCTTCCAAAGGCTGCGAGGAGGAGGAGGAGGAGGAGG 1200

QY 1201 CTTTGAGAACATGGACTACTTTACTCTGGACTTAGAACACATAGCAGAGGCCCTTGAGGGC 1260
DB 1201 CTTTGAGAACATGGACTACTTTACTCTGGACTTAGAACACATAGCAGAGGCCCTTGAGGGC 1260
QY 1261 CATTTGACTTTGGGACAGGTAAAGATGTGATTTACATGTTTACCTTTGAAAGGCAGCG 1320
DB 1261 CATTTGACTTTGGGACAGGTAAAGATGTGATTTACATGTTTACCTTTGAAAGGCAGCG 1320
QY 1321 TTCTCTTTGAGTTCTGAGGGGAACTGTTAAAAAAGTCAAATTTTACACGCCAGTGTGAC 1380
DB 1321 TTCTCTTTGAGTTCTGAGGGGAACTGTTAAAAAAGTCAAATTTTACACGCCAGTGTGAC 1380
QY 1381 AGGTCTCTATAGAGCCCTGACTGTCTTAGTAGTGTCTAAGTAGACCAAGCTGTCTGG 1440
DB 1381 AGGTCTCTATAGAGCCCTGACTGTCTTAGTAGTGTCTAAGTAGACCAAGCTGTCTGG 1440
QY 1441 AACACATAGAGATCTATCTTCCCATCTCTCTTCTTGGGGATGAGATAAAGGCATGT 1500
DB 1441 AACACATAGAGATCTATCTTCCCATCTCTCTTCTTGGGGATGAGATAAAGGCATGT 1500
QY 1501 GCCCACCATGCTGCTCCACAGACAACTTTTGTGATGATCCAGGTTCTGGCAGAGTGC 1560
DB 1501 GCCCACCATGCTGCTCCACAGACAACTTTTGTGATGATCCAGGTTCTGGCAGAGTGC 1560
QY 1561 TGGTACATAATTTGTTTGGAAATAAATTTATCTCGTGCC 1597
DB 1561 TGGTACATAATTTGTTTGGAAATAAATTTATCTCGTGCC 1597

RESULT 3

US-10-775-627-5
; Sequence 5, Application US/10775627
; Publication No. US2004014246A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG:028USD1
; CURRENT APPLICATION NUMBER: US/10775,627
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (299)..(1327)
US-10-775-627-5

Query Match 100.0%; Score 1597; DB 19; Length 1597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCGAGATTACCTTTACAGAACTGTTCCGGAGCACCTTTCCCTTGGCAGCACACTCAG 60
DB 1 CTCGAGATTACCTTTACAGAACTGTTCCGGAGCACCTTTCCCTTGGCAGCACACTCAG 60
QY 61 GGACAGGACCGCAGGAGGAATGACACTTCTCTGAATACAACTCTTCTCCAAAGAGCA 120
DB 61 GGACAGGACCGCAGGAGGAATGACACTTCTCTGAATACAACTCTTCTCCAAAGAGCA 120
QY 121 GCAGACCATGGATAAATCTGGAAAAAGCAACTGATCTGTCTCCCATCTGCCTAGAGATGTTTAC 180
DB 121 GCAGACCATGGATAAATCTGGAAAAAGCAACTGATCTGTCTCCCATCTGCCTAGAGATGTTTAC 180
QY 181 GAAAGCTGTGTGATTTCTCCCTTGGCCAGCAAACTGTGCGAGGAATGTGCGGGCCCCCCC 240

Db 181 ||||| GAAGCCTGTGGTCAATCTCCCTTGCAGCACAACCTGTGCAGGAATGTGCGGCCCCC 240
Qy 241 TTGGAGACAAGACTTGGTGTGACGCGGTGGGCAAGACAGTGCATTTCAAGCAATAT 300
Db 241 TTGGAGACAAGACTTGGTGTGACGCGGTGGGCAAGACAGTGCATTTCAAGCAATAT 300
Qy 301 GGATTATAAATCTAGCCTGATTCCTGATGAAACGCTATGGAACCTGTGAGAAGCAGCT 360
Db 301 GGATTATAAATCTAGCCTGATTCCTGATGAAACGCTATGGAACCTGTGAGAAGCAGCT 360
Qy 361 GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCCTGTGGTCAATCCTGCTGCCAACA 420
Db 361 GATCTGCCCATCTGCTCGAGATGTTTACCAAGCCCTGTGGTCAATCCTGCTGCCAACA 420
Qy 421 CAACCTCTGCCGAAGTGTCCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGAACCA 480
Db 421 CAACCTCTGCCGAAGTGTCCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGAACCA 480
Qy 481 CCGCGGTGGCTCAGTGTCCATGTCGTGAGTGTGTTCCGTTGCGCTCGTGCAGCATGA 540
Db 481 CCGCGGTGGCTCAGTGTCCATGTCGTGAGTGTGTTCCGTTGCGCTCGTGCAGCATGA 540
Qy 541 AGTGATCATGACCGGCA CGGGGTGTACGGCTCTGCAGAGGAACCTGCTGTGGAAAAACAT 600
Db 541 AGTGATCATGACCGGCA CGGGGTGTACGGCTCTGCAGAGGAACCTGCTGTGGAAAAACAT 600
Qy 601 CATTGACATCTACAGCAGAGTGTCCAGTCCGCGCCCTGCAGAAAGGAGCACCAGAT 660
Db 601 CATTGACATCTACAGCAGAGTGTCCAGTCCGCGCCCTGCAGAAAGGAGCACCAGAT 660
Qy 661 GTCAAGGAACACGAAGACGAGAAAGTCAACATCTACTGCTCAGCTGTGAGGTGCTTAC 720
Db 661 GTCAAGGAACACGAAGACGAGAAAGTCAACATCTACTGCTCAGCTGTGAGGTGCTTAC 720
Qy 721 TTGCTCCTTGTGAAAGTGTTCGGGCTCACAGGCTGTGAGGTTCGCCCTTTGCAAG 780
Db 721 TTGCTCCTTGTGAAAGTGTTCGGGCTCACAGGCTGTGAGGTTCGCCCTTTGCAAG 780
Qy 781 CATCTTCCAGGACAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 840
Db 781 CATCTTCCAGGACAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 840
Qy 841 CGACCGAGTGCAGACGATCATCTCAGCTGAGGAGTCTCGTGCAGAGTGAACCAAGAGAA 900
Db 841 CGACCGAGTGCAGACGATCATCTCAGCTGAGGAGTCTCGTGCAGAGTGAACCAAGAGAA 900
Qy 901 TAGCCACCAAGGTGAAGAGGAGCTGAGTCAAGAGTTTGAACCCCTCTACGCCATCTTGA 960
Db 901 TAGCCACCAAGGTGAAGAGGAGCTGAGTCAAGAGTTTGAACCCCTCTACGCCATCTTGA 960
Qy 961 TGAGAGAGAGAGGAGCTGCTGAGCGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
Db 961 TGAGAGAGAGAGGAGCTGCTGAGCGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
Qy 1021 CATCGAGGCTCTGATCTCCTCAGTACAGGAGGAGCTGGAAGTCCCAAGTCTTGA 1080
Db 1021 CATCGAGGCTCTGATCCTCAGTACAGGAGGAGCTGGAAGTCCCAAGTCTTGA 1080
Qy 1081 GACCGCATCCAGTCTGATGAGCCCGAGGAGGAGTACCTTCTCTCAAGTGCAGCA 1140
Db 1081 GACCGCATCCAGTCTGATGAGCCCGAGGAGGAGTACCTTCTCTCAAGTGCAGCA 1140
Qy 1141 GCTCATCAAGAGATGTGAAGCCCTCCAGGAGTCCAGGAGTCCAGGAGTCCAGGAGTCCAG 1200
Db 1141 GCTCATCAAGAGATGTGAAGCCCTCCAGGAGTCCAGGAGTCCAGGAGTCCAGGAGTCCAG 1200
Qy 1201 CTTTGAGAAATCGAATCTTTTACTCTGAGTCTAGAACATAGCAGAGGCTTTGAGGGC 1260
Db 1201 CTTTGAGAAATCGAATCTTTTACTCTGAGTCTAGAACATAGCAGAGGCTTTGAGGGC 1260
Qy 1261 CATTGACTTTGGAGCAGGTAAGGATGTGATGTTTCAATGTTTGAACCTTTGAAGGAGGCG 1320
|||

Db 1261 CATTCAGCTTTGGACACAGGTAAGGATGTGATGTTTCACTGTTGACCTTTGAAAGCAGCG 1320
Qy 1321 TTCTCTCTCAGTCTCTGAGGGAACTGTTAAAAAGTCAAAATTTACACAGCCAGTGTGAC 1380
Db 1321 TTCTCTCTCAGTCTCTGAGGGAACTGTTAAAAAGTCAAAATTTACACAGCCAGTGTGAC 1380
Qy 1381 AGGTCTCTCTATGAGGCCCTGACTGCTCTTAGTAGTGTCTAAAGTAGACCAAGCTGGTCTGG 1440
Db 1381 AGGTCTCTCTATGAGGCCCTGACTGCTCTTAGTAGTGTCTAAAGTAGACCAAGCTGGTCTGG 1440
Qy 1441 AACACATAGAGATCTAATCTTTGCCCATCTCTGCTTTGTAGGGAGATGATAAAGGATGT 1500
Db 1441 AACACATAGAGATCTAATCTTTGCCCATCTCTGCTTTGTAGGGAGATGATAAAGGATGT 1500
Qy 1501 GCGCCACATGCGCTGCCCTCCACAGACAACTTTGTGATGGATCCAGGCTGTGGCAGTGCC 1560
Db 1501 GCGCCACATGCGCTGCCCTCCACAGACAACTTTGTGATGGATCCAGGCTGTGGCAGTGCC 1560
Qy 1561 TGGTACATTAATGTTTTCGAAATAAATTAATCTCGTGCC 1597
Db 1561 TGGTACATTAATGTTTTCGAAATAAATTAATCTCGTGCC 1597

RESULT 4

US-10-061-043A-20
; Sequence 20, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061, 043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: rat
US-10-061-043A-20

Query Match 55.8%; Score 890.8; DB 15; Length 1053;
Best Local Similarity 93.3%; Pred. No. 7.7e-272;
Matches 931; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
Qy 299 ATGGATTATAATCTAGCCTGATTCCTGATGAAACGCTATGGAGAACCTGGAGAACGAG 358
Db 1 ATGGATTATAATCTAGCCTGATTCCTGGACGGAAATGCTATGGAGAACCTGGAGAACGAG 60
Qy 359 CTGATCTGCCCATCTGCTCGCTGGAGATGTTTACCAAGCTGTGTCTATCTGCCCTGCCAA 418
Db 61 CTATCTGCCCATCTGCTCGCTTGGATGTTTACCAAGCTGTGTCTATCTGCCCTGCCAG 120
Qy 419 CACAACCTCTGCGGGAAGTGTGCCACGACATCTTCCAGGCTGCGAATCCCTACTGGAAC 478
Db 121 CACAACCTCTGCGGGAAGTGTGCCACGACATCTTCCAGGCTGCGCAATCCCTACTGGAAC 180
Qy 479 AACCGGCTGCTCAGTGTCCATGTCTGAGGTGCTTTCGTTGCCCTCGTCCGCCCAT 538
Db 181 AACCGGCTGCTCAGTGTCCATGTCTGAGGTGCTTTCGTTGCCCTCGTCCGCCCAT 240
Qy 539 GAAGTGTATCATGGACCGGCACTACGGGTGTACGGCTCTCAGAGGAACCTGCTGTGGAGAAC 598
Db 241 GAAGTGTATCATGGACCGGCACTACGGGTGTACGGCTCTCAGAGGAACCTGCTGTGGAGAAC 300
Qy 599 ATCATTTGACATCTTACAAGCAGGAGTGTCTCCAGTTCGCGCCCTCTGCAGAAAGGACCCCG 658


```

RESULT 6
US-10-061-043A-22
; Sequence 22, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-043A-22

Query Match      50.3%; Score 803.8; DB 15; Length 2097;
Best Local Similarity 86.2%; Pred. No. 4.9e-244;
Matches 889; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 262 GACGCGAGTGGGCAAGACAGTGCATCTTCAAAGCAATATGGATTATAATCTAGCCTGAT 321
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 322 TCCTGATGGAACGCTTATGGAGAACCTGGAGAGCAGCTGATCTGCCCATCTAGCCTGGA 381
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 382 GATGTTTACCAAGCCTGTGTCATCTGCCCTGCCAACAACAACCTCTGCCGGAAGTGTGC 441
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 519 GATGTTTACCAAGCCTGTGTCATCTGCCCTGCCAACAACAACCTCTGCCGGAAGTGTGC 578
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 442 CAAAGCAATCTTCCAGGCTGCGAATCCCTTACTGGACCAACCGGGTGGCTCAGTGCCAT 501
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 579 CAATGACATCTTCCAGGCTGCAATCCCTACTGGACGAGCGGGGAGCTCAGTGTCCAT 638
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 502 GTCTGGAGGTCGTTTCGGTTGCCCTCGCTGCCCGCATGAGTCAATGACGACCGGACCG 561
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 639 GTCTGGAGGCGGTTTCGGCTGCCCCACCTCGCCCGCAGAGGTGATCATGGATCGTCACG 698
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 562 GGTGTACGGCTGCAGAGGAACCTGCTGTGGTGAATAACATCATTTGACATCTACAAGCAG 621
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 699 AGTGTACGGCTGCAGAGGAACCTGCTGTGGTGAATAACATCATTCGACATCTACAAGC 758
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 622 GTGCTCAGTCGGCCCTGCAGAAAGGAGCAGCACCAGTGTGCAAGGAACAAGACGACGA 681
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 759 GTGCTCAGTCGGCCCTGCAGAAAGGAGCAGTCAACCCATGTGCAAGGAGCAGCAAGAT 818
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 682 GAAGATCAACATCTACTGTCTCAGCTGTGAGGTGCTTCTGCTTGTGCAAGGTGTT 741
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 819 GAAATCAACATCTACTGTCTCAGCTGTGAGGTGCTTCTGCTTGTGCAAGGTGTT 778
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 742 TGGGGCTCACAGGCTGTGAGGTGCTTGTGCAAGGTGCTTGTGCAAGGTGTT 801
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 879 TGGGATCCAAAGGCTGCGAGGTGCCCCATTTGCAAGGTGTTTCCAGGACAAAAGAC 938
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 802 TGAGCTGAGTAATCGATCTCCATGTGTGTGGGGGGAACGACCGAGTGCAGATCAT 861
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 939 TGAATGAATAATGTATCTCCATGTGTGTGGGGGGAATGACCGTGTGCAGACCATCAT 998
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 862 CTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGATAGCACAGGTGAAGGAGGA 921
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 999 CACTCAGCTGGAGGATTCCTGCTGAGTGACCAAGGAGAACAGTCAACAGGTAAAGGA 1058
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-10-060-634C-22
; Sequence 22, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-634C-22

Query Match      50.3%; Score 803.8; DB 17; Length 2097;
Best Local Similarity 86.2%; Pred. No. 4.9e-244;
Matches 889; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 262 GACGCGAGTGGGCAAGACAGTGCATCTTCAAAGCAATATGGATTATAATCTAGCCTGAT 321
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 399 GAGGCGAGCTAGGCGTGGCTCTCATCTTCCCAAGCAATGGATTATAAGTTCGAGCCTGAT 458
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 322 TCCTGATGGAACGCTTATGGAGAACCTGGAGAGCAGCTGATCTGCCCATCTAGCCTGGA 381
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 459 CCAGNATGGGATCCCATGAGAGNACTTGGAGAGCAGCTGATCTGCCCTATCTGCCCTGGA 518
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 382 GATGTTTACCAAGCCTGTGTCATCTGCCCTGCCAACAACAACCTCTGCCGGAAGTGTGC 441
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 519 GATGTTTACCAAGCCTGTGTCATCTGCCCTGCCAACAACAACCTCTGCCGGAAGTGTGC 578
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 442 CAAAGCAATCTTCCAGGCTGCGAATCCCTACTGGACGAGCGGGGAGCTCAGTGTCCAT 501
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 579 CAATGACATCTTCCAGGCTGCAATCCCTACTGGACGAGCGGGGAGCTCAGTGTCCAT 638
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 502 GTCTGGAGGTCGTTTCGGTTGCCCTCGCTGCCCGCATGAGTCAATGACGACCGGACCG 561
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 639 GTCTGGAGGCGGTTTCGGCTGCCCCACCTCGCCCGCAGAGGTGATCATGGATCGTCACG 698
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 562 GGTGTACGGCTGCAGAGGAACCTGCTGTGGTGAATAACATCATTTGACATCTACAAGCAG 621
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 699 AGTGTACGGCTGCAGAGGAACCTGCTGTGGTGAATAACATCATTCGACATCTACAAGC 758
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 622 GTGCTCAGTCGGCCCTGCAGAAAGGAGCAGCACCAGTGTGCAAGGAACAAGACGACGA 681
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 759 GTGCTCAGTCGGCCCTGCAGAAAGGAGCAGTCAACCCATGTGCAAGGAGCAGCAAGAT 818
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 682 GAAGATCAACATCTACTGTCTCAGCTGTGAGGTGCTTCTGCTTGTGCAAGGTGTT 741
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 819 GAAATCAACATCTACTGTCTCAGCTGTGAGGTGCTTCTGCTTGTGCAAGGTGTT 778
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 742 TGGGGCTCACAGGCTGTGAGGTGCTTGTGCAAGGTGCTTGTGCAAGGTGTT 801
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 879 TGGGATCCAAAGGCTGCGAGGTGCCCCATTTGCAAGGTGTTTCCAGGACAAAAGAC 938
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 802 TGAGCTGAGTAATCGATCTCCATGTGTGTGGGGGGAACGACCGAGTGCAGATCAT 861
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 939 TGAATGAATAATGTATCTCCATGTGTGTGGGGGGAATGACCGTGTGCAGACCATCAT 998
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 862 CTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGATAGCACAGGTGAAGGAGGA 921
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 999 CACTCAGCTGGAGGATTCCTGCTGAGTGACCAAGGAGAACAGTCAACAGGTAAAGGA 1058
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1000
```

QY 502 GTCTGAGGTCTTTCCGTTGCTTCCGTCCTGTCGCGCCATGAAAGTGATCATGGACCGCACGG 561
DB 639 GTCTGAGGCCGTTTCCGTCGCGCCACCTGCGCCACGAGGTGATCATGGATCGTCAGG 698
QY 562 GTGTACGGCTGACAGAGAACCTGCTGTGTGAAACATCATTTGACATCTCAACAGCAGA 621
DB 699 AGTGTACGGCTGACAGAGAACCTGCTGTGTGAAACATCATTTGACATCTCAACAGCAGA 758
QY 622 GTGCTCCAGTCCGCGCCCTGACAGAAAGGACGACCCGATGTGCAAGGAACACGAAAGAGA 681
DB 759 GTGCTCCAGTCCGCGCTGACAGAGGCGAGTCAACCCATGTCGCAAGGACGACGAGATGA 818
QY 682 GAAGATCAACATCTACTGTCTCACTGTGTGAGGTGCTTACTTGTCTTGTGTGCAAGGTGT 741
DB 819 GAAATCAACATCTACTGTCTCACTGTGTGAGGTGCTTACTTGTCTTGTGTGCAAGGTGT 878
QY 742 TGGGCTCACCAGGCTGTGAGGTGCTTGTGAGGTGCTTGTGAGGTGCTTGTGAGGTGCT 801
DB 879 TGGGATCCACAGGCTGCGAGGTGCTTGTGAGGTGCTTGTGAGGTGCTTGTGAGGTGCT 938
QY 802 TGAGTGTAGTAACTGATCTCCATGCTGTGTGCGGGGAAACGACCGAGTGCAGACGATCAT 861
DB 939 TGAATGTAGTAACTGATCTCCATGCTGTGTGCGGGGAAACGACCGAGTGCAGACGATCAT 998
QY 862 CTCTCAGCTGGAGGACTGTGTGAGGTGCTTGTGAGGTGCTTGTGAGGTGCTTGTGAGGT 921
DB 999 CACTCAGCTGGAGGATTCGCTGAGTGCACCAAGGAGAACAGTCAACAGGTAAAGGAGA 1058
QY 922 GCTGAGTCAGAGTTTGTACACCTCTACGCCATCTTGTGAGGTGCTTGTGAGGTGCTTGT 981
DB 1059 GCTGAGCCAGAGTTTGTACACCTCTTGTGAGGTGCTTGTGAGGTGCTTGTGAGGTGCT 1118
QY 982 GCAGCGGATCACGAGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1041
DB 1119 GCAGCGGATCACGAGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1178
QY 1042 GTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1101
DB 1179 GTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1238
QY 1102 TGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1161
DB 1239 CGAGCTGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1298
QY 1162 AGCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1221
DB 1299 AGCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1358
QY 1222 TACTCTGAGCTTTAGAACACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1281
DB 1359 TACTTTGGATTTAGAGCACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1418
QY 1282 AGATGTGATG 1292
DB 1419 GGAAGAGGAAG 1429

RESULT 8

US-10-221-625-192
; Sequence 192, Application US/10221625
; Publication No. US20040033942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dying Aina M.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom

; APPLICANT: MATHUR, Preete
; APPLICANT: SHAH, Purvi
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: REDDY, Roopa
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: PF-0761 PCT
; CURRENT APPLICATION NUMBER: US/10/221,625
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PERL Program
; SEQ ID NO 192
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040033942A1 3575519CB1
US-10-221-625-192

Query Match 50.2%; Score 802.2; DB 18; Length 1764;
Best Local Similarity 86.1%; Pred. No. 1.5e-243;
Matches 888; Conservative 0; Mismatches 143; Indels 0; Gaps 0;
QY 262 GACGAGCTGGCAAGACAGTCGCATTTCAAAGCAATATGGATTATAATCTAGCCTGAT 321
DB 86 GAGGAGCTAGCGGTGCTCTCATTTCTCCACAGAATGGATTATAAGTCGAGCCTGAT 145
QY 322 TCCTGATGAAACGCTATGGAGAACCTGGAGAACGAGCTGATCTGCCCCATCTGCTCGA 381
DB 146 CCAGATGGGATCCATGGAGAACTTGGAGNAGCAGCTGATCTGCCCTATCTGCTCGA 205
QY 382 GATGTTTACCAGCTGTGGTATCCTGCTGCTGCAACAACTCTGCGGAAAGTGTGC 441
DB 206 GATGTTTACCAGCTGTGGTATCCTGCTGCTGCAACAACTCTGCGGAAAGTGTGC 265
QY 442 CAACGACATCTTCCAGGCTGGAAATCCCTACTTGGACCAACCGCGTGGCTCAGTGTCCAT 501
DB 266 CAATGACATCTTCCAGGCTGGAAATCCCTACTTGGACCAACCGCGTGGCTCAGTGTCCAT 325
QY 502 GTCTGAGGTCTTTCGTTGCTTGCCTGCTGCGCCATGAAGTGATCATGGACCGGACCG 561
DB 326 GTCTGAGGCGCTTTCGCTGCGCCACCTGCGCCACGAGGTGATCATGGATCGTCACGG 385
QY 562 GTGTACGCGCTGACAGAGAACTCTGCTGTGTGAAACATCATTTGACATCTCAAGCAGA 621
DB 386 AGTGTACGCGCTGACAGAGAACTCTGCTGTGTGAAACATCATTCGACATCTCAAAACAGA 445
QY 622 GTGCTCCAGTCCGCGCTGACAGAGGCGAGTCAACCCATGTGCAAGGAGCAGAAAGATGA 505
DB 446 GAAGATCAACATCTACTGTCTCACGTGTGAGGTGCTTACTTGTCTTGTGCAAGGTGT 741
QY 506 GAAATCAACATCTACTGTCTCACGTGTGAGGTGCTTACTTGTCTTGTGCAAGGTGT 565
QY 742 TGGGCTCACCAGGCTGTGAGGTGCTTGTGAGGTGCTTGTGAGGTGCTTGTGAGGTGCT 801
DB 566 TGGGATCCACAGGCTGCGAGGTGCTTGTGAGGTGCTTGTGAGGTGCTTGTGAGGTGCT 625
QY 802 TGAGTGTAGTAACTGATCTCCATGCTGTGTGCGGGGAAACGACCGAGTGCAGACGATCAT 861
DB 626 TGAATGAATTAATGATCTCCATGCTGTGTGCGGGGAAATGACCGTGTGTCAGACCATCAT 685
QY 862 CTCTCAGCTGGAGGACTCTGTGACAGAGTGCACCAAGGAGAAATAGCCACAGTGAAGGAGA 921
DB 686 CACTCAGCTGGAGGATTCGCTGAGTGCACCAAGGAGAAACAGTCAACAGGTAAAGGAGA 745
QY 922 GCTGAGTCAGAGTTTGCACACCTCTTACGCCATCTCTGAGTGAAGAAAGAGGAGGTGCT 981
DB 746 GCTGAGCCAGAGTTTGCACACCTCTTACGCCATCTCTGAGTGAAGAAAGTGAAGTGTCT 805
QY 982 GCAGCGGATCACGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1041

Dd	806	GCACGGGATCACGAGGAGCAGGAGAAAAGCTTAGCTTCATCGAGGCCCTCATCCAGCA	865
Qy	1042	GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA	1101
Dd	866	GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA	925
Qy	1102	TGACCCGGAGGGGCTACCTTCTCTCAAGTGCACAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA	1161
Dd	926	CGAGCCTGGGGAGCCACCTCTCTTGTAGTGCACAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA	985
Qy	1162	AGCCTCCAAAGGGTGCAGCTGGGGAAGACAGAGCAAGGCTTGTGGAGACCGCCATCCAGTCCCTGGA	1221
Dd	986	AGCTTCCAAAGGGTGCAGCTGGGGAAGACAGAGCAAGGCTTGTGGAGACCGCCATCCAGTCCCTGGA	1045
Qy	1222	TACTCTGGACTTAGAACACATAGCAGAGCCTTGTGGAGACCGCCATCCAGTCCCTGGA	1281
Dd	1046	TACTTTGGATTTAGAGCACAATAGCAGAGCCTTGTGGAGACCGCCATCCAGTCCCTGGA	1105
Qy	1282	AGGATGTGATG 1292	
Dd	1106	GGAGAGGAAG 1116	
RESULT 9			
US-10-723-860-7801			
; Sequence 7801, Application US/10723860			
; Publication No. US20040253606A1			
; GENERAL INFORMATION:			
; APPLICANT: Aziz, Natasha			
; APPLICANT: Ginsburg, Wendy M.			
; APPLICANT: Zlotnik, Albert			
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &			
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators			
; FILE REFERENCE: 05882.0193.NPUS01			
; CURRENT APPLICATION NUMBER: US/10/723,860			
; CURRENT FILING DATE: 2003-11-26			
; PRIOR APPLICATION NUMBER: 60/429,739			
; PRIOR FILING DATE: 2002-11-26			
; NUMBER OF SEQ ID NOS: 8393			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 7801			
; LENGTH: 2700			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-723-860-7801			
Query Match			
Best Local Similarity 50.2%; Score 802.2; DB 20; Length 2700;			
Matches 888; Conservative 0; Mismatches 143; Indels 0; Gaps 0;			
Qy	262	GACGAGGTGGGCAAGACAGATCGCATTTCAAAGCAATATGGATTATAAATCTAGCCCTGAT	321
Dd	992	GAGGAGCTAGGGCTGGCTCTCATCTCCCAAGAAATGGATTATAAGTGGAGCCCTGAT	1051
Qy	322	TCCTGTGGAACCGCTATGAGAACCTTGGAGAGCAGCTGATCTGCCCATCTGCTCGGA	381
Dd	1052	CCAGGATGGAAATCCCATGGAGAACTTGGAGAGCAGCTGATCTGCCCTATCTGCTCGGA	1111
Qy	382	GATGTTTACCAAGCCTGTGTGATCTGCTGCCCAACAACTCTGCCGGAAGTGTGC	441
Dd	1112	GATGTTTACCAAGCCTGTGTGATCTGCTGCCCAACAACTCTGCCGGAAGTGTGC	1171
Qy	442	CAACGACATCTCCAGGCTGCGAATCCCTACTGAGCAACCGGGTGGCTCAGTGTCCAT	501
Dd	1172	CAATGACATCTCCAGGCTGCGAATCCCTACTGAGCAACCGGGTGGCTCAGTGTCCAT	1231
Qy	502	GTCTGGAGTGTGTTCCGTTGGCCCTCGTGGCCCATGAAGTATCATGACCGGACCG	561
Dd	1232	GTCTGGAGTGTGTTCCGTTGGCCCTCGTGGCCCATGAAGTATCATGACCGGACCG	1291
Qy	562	GGTGTAGGGCTGCAGAGGAACCTGCTGGTGGAAAACATCATTTGACATCTACAGCAGGA	621
Dd	1292	AGTGTAGGGCTGCAGAGGAACCTGCTGGTGGAAAACATCATTCGATCTTACAAACAGGA	1351
Qy	622	GTGCTCCAGTCCGCCCCCTGCAGAAAAGGAGCCACCGATGTGCAAGGAAACACGAGACGA	681
Dd	1352	GTGCTCCAGTCCGCCCCCTGCAGAAAAGGAGCCACCGATGTGCAAGGAAACACGAGATGA	1411
Qy	682	GAAGATCAACTACTACTGTCTCACGTGTGAGTGCTTACTTCTCTTGTGCAAGGTGTT	741
Dd	1412	GAAGATCAACTACTACTGTCTCACGTGTGAGTGCTTACTTCTCTTGTGCAAGGTGTT	1471
Qy	742	TGGGGCTCACCAAGGCTGTGAGTGTGCCCCCTTGCANAAGCATCTTCCAAAGGACAGAGAC	801
Dd	1472	TGGGGCTCACCAAGGCTGTGAGTGTGCCCCCTTGCANAAGCATCTTCCAAAGGACAGAGAC	1531
Qy	802	TGAGCTGAGTAACTGATCTCTCATGCTGTGTGCGGGGAACCGAGTGCAGACGATCAT	861
Dd	1532	TGAGCTGAGTAACTGATCTCTCATGCTGTGTGCGGGGAACCGAGTGCAGACGATCAT	1591
Qy	862	CTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGAGGAATAGCCACAGGTGAAGGAGA	921
Dd	1592	CACTCAGCTGGAGGATTCCTCGTGTGACCAAGGAGAACAGTCAACAGGTAAAGGAAGA	1651
Qy	922	GCTGAGTCAAGAGTTTGACACCTCTACGCCATCTCGAGTGCAGAGGCTCTGATCCTCCA	1041
Dd	1652	GCTGAGTCAAGAGTTTGACACCTCTGATGCCATCTCGAGTGCAGAGGCTCTGATCCTCCA	1711
Qy	982	GCAGCGGATCACGAGGAGCAGGAGGAGAAAGCTGGGCTTTCATCGAGGCTCTGATCCTCCA	1041
Dd	1712	GCAGCGGATCACGAGGAGCAGGAGGAGAAAGCTGGGCTTTCATCGAGGCTCTGATCCTCCA	1771
Qy	1042	GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA	1101
Dd	1772	GTACAGGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGA	1831
Qy	1102	TGAGCCCGAGGGGCTACCTTCTCTCAAGTGCAGAGCAGCTCATCAAGAGCATTTGTAGA	1161
Dd	1832	CGAGCCTGGGGAGGCCACCTTCTCTTGTACTGCCAAGCAACTCATCAAAAGCATTTGTGGA	1891
Qy	1162	AGCCTCCAAAGGCTGCGAGCTGGGGAAGACAGAGCAAGGCTTGTGAAACATGGACTACTT	1221
Dd	1892	AGCTTCCAAAGGCTGCGAGCTGGGGAAGACAGAGCAAGGCTTGTGAAACATGGACTACTT	1951
Qy	1222	TACTCTGGACTTAGAACACATAGCAGAGCCCTTGGAGGCTTGTGAGGACAGGTAA	1281
Dd	1952	TACTTTGGATTTAGAGCACAATAGCAGAGCCCTTGGAGGCTTGTGAGGACAGGTAA	2011
Qy	1282	AGGATGTGATG 1292	
Dd	2012	GGAGAGGAAG 2022	
RESULT 10			
US-10-094-749-1222			
; Sequence 1222, Application US/10094749			
; Publication No. US20030219741A1			
; GENERAL INFORMATION:			
; APPLICANT: ISOGAI, TAKAO			
; APPLICANT: SUGIYAMA, TOMOYASU			
; APPLICANT: OTSUKI, TETSUJI			
; APPLICANT: WAKAMATSU, AI			
; APPLICANT: SATO, HIROYUKI			
; APPLICANT: ISHII, SHIZUKO			
; APPLICANT: YAMAMOTO, JUN-ICHI			
; APPLICANT: ISONO, YUUKO			
; APPLICANT: HIO, YURI			
; APPLICANT: OTSUKA, KAORU			
; APPLICANT: NAGAI, KEIICHI			
; APPLICANT: IRIE, RYOTARO			
; APPLICANT: TAMECHIKI, ICHIRO			
; APPLICANT: SEKI, NAOHICO			
; APPLICANT: YOSHIKAWA, TSUTOMU			
; APPLICANT: OTSUKA, MOTOYUKI			
; APPLICANT: NAGAHARI, KENJI			
; APPLICANT: MASUHO, YASUHIKO			


```
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1222
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-1222

Query Match      50.1%; Score 800.6; DB 17; Length 1764;
Best Local Similarity 86.0%; Pred. No. 4.7e-243;
Matches 887; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 262 GACGAGGTGGGCAAGACAGATCGCATTTCAAAGCAATATGGATTATAAATCTAGCCTGAT 321
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 100 GAGGAGCTAGCGTGGCTCTATTCTTCCACAGATGGATTATAAGTCAGCTGAT 159
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 322 TCCTGATGAAACGCTATGGAGAACTGGAGAAAGCAGCTGATCTGCCCATCTGCTCGA 381
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 160 CCAGGATGGAAATCCCATGGAGAACTTGAGAAAGCAGCTGATCTGCCCTATCTGCTCGA 219
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 382 GATGTTTACCAGCCTGTGTTCTATCTCTCCCTGCCCAACACACACTCTGCCGGAAGTGC 441
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 220 GATGTTTACCAGCAGTGGTCTATCTTGGCGTGCAGACACAACTGTGCCGGAAGTGC 279
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 442 CAACGACATCTTCCAGGCTCGAAATCCCTACTCGGACCAACCGCGTGGCTCAGTGTCCAT 501
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 280 CAATGACATCTTCCAGGCTGCAATCCCTACTTGGACCAACCGCGTGGCTCAGTGTCCAT 339
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 502 GTCTGAGGTGCTTTCCGTTGCCCCCTGCGCCCATGAAGTGATCATGGACCCGACCG 561
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 340 GTCTGAGGCCGTTTCCGCTGCCCCACCTGCGCCACGAGGTGATCATGGATCGTCACGG 399
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 562 GTGTACGGCTGCGAGAGGAACCTGCTGGTGGAAACATCATTTGACATCTACCAAGCA 621
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 400 AGTTTACGCGCTGCGAGAGGAACCTGCTGGTGGAGAACATCATTCGACATCTACAAACAG 459
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 622 GTGCTCCAGTGGCGCCCTGCGAGAGGAGCAGCCAGCGATGTGCAAGGAACACGAAGACGA 681
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 460 GTGCTCCAGTGGCGCGCTGCGAGAGGAGCAGTCCACCCATGTGCAAGGACACGAAGATGA 519
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 682 GAAATCAACATCTACTGTCTCACGTGTGAGTGGCTTACTTGTCTTGTGCAAGGTGT 741
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 520 GAAATCAACATCTACTGTCTCACGTGTGAGTGGCTTACTTGTCTTGTGCAAGGTGT 579
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 742 TGGGCTCACAGGCTGTGAGTGGCTTGTGCAAGGACATCTTCCAAGGACAGAAAGAC 801
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 580 TGGGATCCACAAAGGCTGCGAGGTGGCCCCATTGCAAGAGTGTCTTCCAAGGACAAAGAG 639
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 802 TGAGCTGAGTAATCTGATCTTCAATGCTGGTGGGGAACGACCGAGTGCAGACCATCAT 861
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 640 TGAATGAATACTGTAATCTTCAATGCTGGTGGGGAATGACCGTGTGCAAGACCATCAT 699
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 862 CTCTCAGCTGGAGGACTCGTGAGAGTGACCAAGGAGAAATAGCCACCGAGGTGAAGGAGA 921
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 700 CACTCAGCTGGAGGATTCGCTGAGTGACCAAGGAGAAACAGTCAACAGGTAAAGGAAGA 759
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 922 GCTGATGCAAGATTGTAACACCTCTACCGCATCTCTGATGAGAAAGAGGAGGAGCTGCT 981
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 760 GCTGAGCCAGAAAGTTGTAACACCTCTGATGCCATCTCTGATGAGAAAGAAAGTGTGCT 819
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 982 GCAGCGGATCACGAGGAGCAGGAGAAAGCTGGGCTTCTATCGAGGCTCTGATCCTCCA 1041
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 820 GCAGCGGATCACGAGGAGCAGGAGAAAGCTTATAGCTTCTATCGAGGCGCTCATCCAGCA 879
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1042 GTACAGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTCGA 1101
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


Db 502 GAAAAATAACATCTACTGTCTCTCACTGTGTGAGTGCCACCTGCTCCATGTGCAAGGTGTT 561
QY 742 TGGGGCTCACAGGCTGTGAGGTGCCCCCTTTGCAAGCATCTTCCAAAGCAGAGAC 801
Db 562 TGGGATCCAAAGGCTTGCAGGTGGCCCCATTTGAGAGTGTCTTCCAGGCAAAAGAC 621
QY 802 TGAGCTGAGTAATGCTATCTCCATGTGTGTGGGGGAACGACCGAGTGCAGACGATCAT 861
Db 622 TGAATGAATAATGTATCTCCATCTGTGTGGCGGGGAATGACCGTGTGCAGACCATCAT 681
QY 862 CTCTAGCTGGAGGACTCTGTGAGAGTAGCAAGAGAGATAGCCACAGGTGAAGGAGA 921
Db 682 CACTCAGCTGGAGGATTTCCCGTCGAGTGACCAAGAGAAACAGTCACCAAGGTAAAGGA 741
QY 922 GCTGAGTCAGAGTTTGACACCTCTACGCCATCTCTGGATGAGAAAGAGCGAGCTGCT 981
Db 742 GCTGAGCCAGAGTTTGACACGTTGTATGCCATCTCTGGATGAGAAAGATGAGTGTCT 801
QY 982 GCAGCGGATCACGAGGAGGAGGAGAGCTGGGCTTCATCGAGGCTCTGATCCTCCA 1041
Db 802 GCAGCGGATCACGAGGAGGAGGAGAAAGCTTAGCTTCATCGAGGCCCTCATCCAGCA 861
QY 1042 GTACAGGAGCAGCTGAAAGTCCACCAAGCTTGTGGAGACCGGCATCCAGTCCCTGGA 1101
Db 862 GTACAGGAGCAGCTGACCAAGTCCACCAAGCTTGTGGAACTGCCATCCAGTCCCTGGA 921
QY 1102 TGAGCCGGAGGGGCTACCTTCTCTCAAGTGCCAAAGCAGCTCATCAAGAGCATTGAGA 1161
Db 922 CGAGCTTGGGGAGCCACCTTCTCTTGACTGCTCAAGCAACTCATCAAAGCATTTGGA 981
QY 1162 AGCTTCCAAGGGCTGCGAGCTGGGGAAGAGCAGACCAAGGCTTTGAGAATCGACTACTT 1221
Db 982 AGCTTCCAAGGGCTGCGAGCTGGGGAAGAGCAGAGCAGGGCTTTTGAGAACATGGACTTCT 1041
QY 1222 TACTCTGACTTAGACACATAGCAGAGGCTTGAAGGCCATTTGACTTTGGGACAGGTA 1281
Db 1042 TACTTTGGATTTAGACACATAGCAGCGCCCTTGAGAGCCATTTGACTTTGGGACAGATGA 1101
QY 1282 AGGATGTGATG 1292
Db 1102 GGAAGGAGAG 1112

RESULT 12

US-10-204-921-12

; Sequence 12, Application US/10204921

; Publication No. US2005009587A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: PANZER, Scott R.

; APPLICANT: SPIRO, Peter A.

; APPLICANT: BANVILLE, Steven C.

; APPLICANT: SHAH, Purvi

; APPLICANT: CHALUP, Michael S.

; APPLICANT: CHANG, Simon C.

; APPLICANT: CHEN, Alice

; APPLICANT: D'SA, Steven A.

; APPLICANT: AMSHEY, Stefan

; APPLICANT: DAHL, Christopher R.

; APPLICANT: DAN, Tam C.

; APPLICANT: DANIELS, Susan E.

; APPLICANT: DUFOUR, Gerard E.

; APPLICANT: FLORES, Vincent

; APPLICANT: FONG, Willy T.

; APPLICANT: GREENAWALT, Lila B.

; APPLICANT: HILLMAN, Jennifer L.

; APPLICANT: JONES, Anissa L.

; APPLICANT: LIU, Tommy F.

; APPLICANT: ROSEBERRY, Ann M.

; APPLICANT: ROSEN, Bruce H.

; APPLICANT: RUSSO, Frank D.

; APPLICANT: STOCKDREHER, Theresa K.

; APPLICANT: DAFFO, Abel

; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: COHEN, Howard J.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Stephen E.
; APPLICANT: JACKSON, Stuart
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1133 PCT
; CURRENT APPLICATION NUMBER: US/10/204,921
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/185,213; 60/205,285; 60/205,232; 60/205,323; 60/205,287;
; 60/205,324; 60/205,286
; PRIOR FILING DATE: 2000-02-24; 2000-05-17; 2000-05-16; 2000-05-17; 2000-05-17;
; 2000-05-17; 2000-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 2110
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LG-247384.1:2000MAY19
US-10-204-921-12

Query Match 46.8%; Score 747.8; DB 21; Length 2110;
Best Local Similarity 82.8%; Pred. No. 3.1e-226;
Matches 854; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 262 GACGAGGTGGGCAAGACAGTCGCATTTCAAAGCAATATGGATTATAAATCTAGCCTGAT 321
Db 88 GAGGAGCTAGGCGTGGCTCTCATTCCTTCCACAGAATGGATTATAAGTCGAGCCTGAT 147
QY 322 TCTGATGAAACGGCTATGGAGAACTGGAGAAAGCAGCTGATCTGCCCATCTGCCCTGGA 381
Db 148 CCAGGATGGGATCCCATGGAGAACTTGGAGAAAGCAGCTGATCTGCCCTATCTGCCCTGA 207
QY 382 GATGTTTACCAAGCCTGTGTCTATCTGCCCTGCCAAACAACACCTCTGCCGGAAGTGTGC 441
Db 208 GATGTTTACCAAGCAGTGTCTATCTTGGCGTGCCAGCACAACCTGTGCCGAAGTGTGC 267
QY 442 CAACGACATCTTCCAGGCTGCGAATCCCTACTTGGACCAACCGGGTGGCTCAGTGTCCAT 501
Db 268 CAATGATATTTTCCAGGCTCTTAACCCGTATTGCCCCCAAGAGGAGGTACCAACCATGGC 327
QY 502 GTCTGGAGGTGCTTTTCCGTTGCCCTCGTGCCGCAATGAAGTGATCATGGACCGGCACGG 561
Db 328 ATCAGGGGCGGATTCGCTGCCATCTCTGTAGACATGAAGTGGTTTGGATAGACATGG 387
QY 562 GGTGTAACGCTGTCAGAGGAACTGCTGTGTGAAACATCATTTGACATTTAAGCAGGA 621
Db 388 GGTATATGGAATTCAGAGGAACTGCTGTGTGAGAAACATCATCGACATCTACAAACAGGA 447
QY 622 GTGCTCCAGTCGGCCCCCTGCAGAAAGGACGACCCGATGTCCAGGAAACAGGACGAGCA 681
Db 448 GTGCTCCAGTCGGCGCGCTGCAGAAAGGAGTCAACCCCATGTGCAAGGAGCAGGATGA 507
QY 682 GAAGATCAACATCTACTGTCTCACTGTGAGGTGCCCTACTTGTCTCTTGTCAAGGTGTT 741
Db 508 GAAATCAACATCTACTGTCTCACTGTGAGGTGCCACCTGCTCATGTGCAAGGTGTT 567
QY 742 TGGGGCTCACAGGCTGTGAGGTGCCCTTTGAAAGCATCTTCCAAAGGACAGAAAGAC 801
Db 568 TGGGATCCCAAGGGCTGCGAGGTGGCCCCCATTTGCAAGTGTCTTCCAGGGACAAAAGAC 627
QY 802 TGAGCTGAGTAATGCTATCTCCATCTCCATCTGCTGGTGGGGGAACGACCGAGTGCAGACGATCAT 861
Db 628 TGAACCTGAATAACTGTATCTCCATCTGCTGGTGGGGGAATGACCCGTGTGCAGACCATCAT 687

QY 862 CTCTCAGCTGGAGGACTCGTGCAGAGTGCACCAAGAGAAATAGCCACAGGTTGAAGGAGA 921
DB |||||
QY 688 CACTCAGCTGGAGGATTCCTCGAGTGCACCAAGAGAAACAGTCAACAGGTAAGGAGA 747
DB |||||
QY 922 GCTGAGTCAGAGTTTGCACACCTCTACGCCATCTGGATGAGAGAGAGAGAGTCTGCT 981
DB |||||
QY 748 GCTGAGCCAGAAAGTTTGACACCTTGTATGCCATCTGGATGAGAGAAAGTGTGCT 807
DB |||||
QY 982 GCAGCGGATCACGAGGAGCAGAGGAGAAAGCTGGGCTTCATCGAGGCTCTGATCCTCCA 1041
DB |||||
QY 808 GCAGCGGATCACGAGGAGCAGAGGAGAAAGCTTAGCTTCATCGAGGCCCTCATCCAGCA 867
DB |||||
QY 1042 GTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGAGAGCCGCATCCAGTCCCTGGA 1101
DB |||||
QY 868 GTACAGGAGCAGCTGGCAAGTCCACAAAGCTGGTGGAAATCGCCATCCAGTCCCTGGA 927
DB |||||
QY 1102 TGAGCCCGAGGGCTACCTCTCAAGTCCCAAGCAGCTCATCAAGAGCATTTGAGA 1161
DB |||||
QY 928 CGAGCCTGGGGAGCCACTTCTTGACTCCCAAGCAACTCATCAAGCAATTTGTGA 987
DB |||||
QY 1162 AGCCTCCAGGGCTGCCAGCTGGGGAAGACAGAGCAAGGCTTTGAGAAACATGGACTACTT 1221
DB |||||
QY 988 AGCTTCCAGGGCTGCCAGCTGGGAGACAGAGCAGGGCTTTGAGAAACATGGACTTCTT 1047
DB |||||
QY 1222 TACTCTGACTTAGAACACATAGCAGAGGCTTTGAGGGCCATTTGAGGACAGGTAA 1281
DB |||||
QY 1048 TACTTTGGATTAGAGCACATAGCAGAGCCCTGAGAGCCATTTGAGGACAGATGA 1107
DB |||||
QY 1282 AGGATGTGATG 1292
DB |||||
QY 1108 GGAAGAGGAAG 1118
DB |||||

RESULT 13

US-10-061-043A-32
; Sequence 32, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 630
; TYPE: DNA
; ORGANISM: rat
US-10-061-043A-32

Query Match 34.3%; Score 547.4; DB 15; Length 630;
Best Local Similarity 94.0%; Pred. No. 8.6e-163;
Matches 569; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 295 CAATATGGATTATAAATCTAGCTGATTCCTGATGGAAACGCTATGGAGAACCTCGAGAA 354
DB |||||
QY 21 CGACAAAGATTATAAATCTGGCTTGATTCGGACCGAAATGCTATGGAGAACCTCGAGAA 80
DB |||||
QY 355 GCAGCTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGGTCACTCCCTCG 414
DB |||||
QY 81 GCAGCTCATCTGCCCATCTGCTTTGAGATGTTTACCAAGCCTGTGGTCACTCCCTCG 140
DB |||||
QY 415 CCAACAAACCTCTGCCGGAAGTGTGCCAACACATCTTCAGGCTGCGAATCCCTACTG 474
DB |||||
QY 141 CCAGACAAACCTCTGCCGGAAGTGTGCCAACACATCTTCAGGCTGCGAATCCCTACTG 200
DB |||||

RESULT 14

US-10-060-634C-32
; Sequence 32, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 630
; TYPE: DNA
; ORGANISM: rat
US-10-060-634C-32

Query Match 34.3%; Score 547.4; DB 17; Length 630;
Best Local Similarity 94.0%; Pred. No. 8.6e-163;
Matches 569; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 295 CAATATGGATTATAAATCTAGCTGATTCCTGATGGAAACGCTATGGAGAACCTCGAGAA 354
DB |||||
QY 21 CGACAAAGATTATAAATCTGGCTTGATTCGGACCGAAATGCTATGGAGAACCTCGAGAA 80
DB |||||
QY 355 GCAGCTGATCTGCCCATCTGCTGGAGATGTTTACCAAGCCTGTGGTCACTCCCTCG 414
DB |||||
QY 81 GCAGCTCATCTGCCCATCTGCTTTGAGATGTTTACCAAGCCTGTGGTCACTCCCTCG 140
DB |||||
QY 415 CCAACAAACCTCTGCCGGAAGTGTGCCAACACATCTTCAGGCTGCGAATCCCTACTG 474
DB |||||

Db 141 CCAGCAAACTCTGCGGAAGTGTGCCAAGCATCTTCCAGCTGCCAATCCCTACTG 200
Qy 475 GACCAACCGGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTTCGGTTCGCCCTCGTGGCG 534
Db 201 GACCAACCGGGTGGCTCAGTGTCCATGTCTGGAGTCTGTTTCGGTTCGCCCTCGTGGCG 260
Qy 535 CCATGAAGTATCATGACCGGCAACCGGGGTGTACGGCTCTGCAGAGAACTCTGCTGGTGA 594
Db 261 CCATGAAGTATCATGACCGGCAACCGGGGTGTACGGCTCTGCAGAGAACTCTGCTGGTGA 320
Qy 595 AAACATCAATGACATCTAAGCAGAGTGTCTCAGTGGCCCTCTGCAGAAAGCGACCA 654
Db 321 GAAATCATCATGATCTTCAAGCAGGAATCTCAGTGGCCCTCTGCAGAAAGCGACCA 380
Qy 655 CCCGATGTGCAAGGAACCAAGACGAGAGATCAACATCTACTGTCTCAGCTGAGGT 714
Db 381 CCCGATGTGCAAGGAACCAAGACGAGAAATCAACATCTACTGTCTCAGCTGAGGT 440
Qy 715 GCCTACTTGTCTCTGTGCAAGGTGTTTGGGGCTCACCAAGCTGTGAGGTTCGCCCTTT 774
Db 441 GCCTACTTGTCTCTGTGCAAGGTGTTTGGGGCTCACCAAGCTGTGAGGTTCGCCCTTT 500
Qy 775 GCAAGCATCTTCCAGGACAGAACTGAGCTGAGTAACTGATCTCCATGCTGTGTGC 834
Db 501 ACAAGCATCTTCCAGGACAGAACTGAACTGAGCAATTGCATCTCCATGCTGTGTGC 560
Qy 835 GGGGAACGACCGAGTGACAGCATCTCTCAGCTGGAGACTCTGTCAGAGTGAACCA 894
Db 561 AGGGAACGACCGAGTTTCACTATCTCCAGCTGGAGACTCTGCGAGTGAACCA 620
Qy 895 GGAGA 899
Db 621 GGTGA 625

RESULT 15
US-09-908-988B-1
; Sequence 1, Application US/09908988B
; Patent No. US20020127690A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028US
; CURRENT APPLICATION NUMBER: US/09/908, 988B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1296)
US-09-908-988B-1

Query Match 30.3%; Score 484.6; DB 9; Length 1431;
Best Local Similarity 69.2%; Pred. No. 1.2e-142;
Matches 677; Conservative 0; Mismatches 299; Indels 3; Gaps 1;
Qy 317 CTGATTCCTGATGGAACGCTATGGAGAACCTTGGAGACGAGCTGATCTGCCCATCTGC 376
Db 226 CTGCTAGGGATGGCACAACATGGACAACCTTGGAGAGAGCTATTTGCCCATCTGC 285
Qy 377 CTGAGATGTTTACCAAGCTGTGGTCACTCTGCCCTGCCAACAACCTCTGCCGGAAG 436
Db 286 CTGAGATGTTTCCAAAGCCCGTGGTCACTTGGCTGCCAACAACCTGTGCCCAAG 345
Qy 437 TGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGCGGTGGCTCAGTG 496

Db 346 TGTGCCAACGACGCTCTTCCAGGCTCTAATCTCTCTGTGCAATCCCGGGCTCCACAACG 405
Qy 497 TCCATGTCTGGAGTCTGTTTCGGTTCGCCCTCGTGGCCGCAATGAAGTATCATGACCGG 556
Db 406 GTGTCTTCCAGGAGCGTTCGGATGCCCATCTTGTAGGACGAGGTTTCTCTGGCAGG 465
Qy 557 CACGGGCTGTACGGCTCTCAGAGAACCTTCTGGTGGAAAAACATCATTTGACATCTCAAG 616
Db 466 CATGTGTCTATGGCCCTCAGCGGAACCTTGTAGTGGAGAAACATCATTTGACATCTCAAG 525
Qy 617 CAGGAGTGTCTCCAG---TCGGGCCCTGCAGAAAGCGACGCCCATGTGCAAGAACAC 673
Db 526 CAGGAGTCTCTCCGGCCACTGCACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCAC 595
Qy 674 GAAGACGAAAGTCAACATCTACTGTCTCAGTGTGAGGTGCTACTTGTCTCTGTGTGC 733
Db 586 GAGGACGAAAGTCAACATCTACTGTCTGAGTGTGAGGTGCGCCCTCTGCCCCACCATTTACAACGC 645
Qy 734 AAGGTCTTTGGGGCTCACCAAGGCTGTGAGGTGCGCCCTTTGCAAAAGCATCTTCCAAGGA 793
Db 646 AAGGTCTTGGGCCCAAGGACTGTGAGGTGCGCCCTCTGCCCCACCATTTACAACGC 705
Qy 794 CAGAAAGTGAAGTGAAGTAACTCTCCATCTGCTGTGTCGGCGGGAAACGACCGAGTGCA 853
Db 706 CAGAAAGTGAAGTGAAGTAACTCTGCGCATCGCATGTGCTGTGCGGGCAATGACCGTGTGCAG 765
Qy 854 ACGATCATCTCTCAGCTGAGGACTCTGTCAGAGTGAACCAAGGAGATAGCCACGAGTG 913
Db 766 GCAGTGAATCACCACGATGGAGGAGGTGTGCCAGACCATTTGAGGACAAACAGCCGACAGAC 825
Qy 914 AAGGAGGAGCTGAGTCAGAAAGTTTGACACCTCTACGCCATCTCTGATCAGAAAGAGC 973
Db 826 AAGCAACTGTTAAACAGAGGTTTCAGACCTCTGTGCGCGTTTGGAGAGGCCAAGGGC 885
Qy 974 GAGCTGTCCAGCGGATCAGCAGGACGAGGAGGAGAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAG 1033
Db 886 GAACTGCTTCAAGCACTGGCCCGGAGCAGGAGGAGAAAGTTGCAGCGCTGCGGGGCTC 945
Qy 1034 ATCTCTCAGTACAGGAGCAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAG 1093
Db 946 ATCCGCGAGTACGAGAGACCACTTGGAGGGCTCTCTCAAGCTGTGGAGTCCCGCATCCAG 1005
Qy 1094 TCCTGTGATGAGCCCGAGGGCTACTTCTCTCAAGTGCCAAAGCAGCTCATCAAGAGC 1153
Db 1006 TCCATGGAGAGCGCCAGATGCTCTTACTCTCAGCAGCAAGAGAGCTGATCAACAG 1065
Qy 1154 ATTGTAGAAGCTTCAAGGGCTGCCAGCTGGGGAGACAGAGCAAGCTTTTGAAGACATG 1213
Db 1066 GTCGGGGCAATGTCGAAAGTGGAGCTGGCAGGACCGCCGAGCGAGGCTATGAGAGCATG 1125
Qy 1214 GACTACTTCTTCTGGAATAGAACATAGCAGAGGCTTGGAGGCTTGAAGCTTTGGG 1273
Db 1126 GAGCAATCTCTGTGAGCGTGGAGCAGTGGCGGCAAAATGTTCGAACCATCGACTTCCAG 1185
Qy 1274 ACAGGTAAAGGATGTGATG 1292
Db 1186 CCGGGCGCGCTGGGGATG 1204

RESULT 16
US-10-775-649-1
; Sequence 1, Application US/10775649
; Publication No. US20040132160A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028US2
; CURRENT APPLICATION NUMBER: US/10/775,649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988

```
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1296)
US-10-775-649-1

Query Match      30.3%; Score 484.6; DB 19; Length 1431;
Best Local Similarity 69.2%; Pred. No. 1.2e-142;
Matches 677; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

QY 317 CTGATTCCTGATGGAAACCTATGGAGAACCTGGAGAACGACGCTGATGCCCCATCTGC 376
DB |||||
QY 226 CTGCTAGGGGATGGCAACATGACAACTTGGAGAACGCTCATTTGCCCCATCTGC 285
DB |||||
QY 377 CTGGAGATGTTTACCAAGCCTGTGTCATCTCTGCTCCCTGCGCAATGATGATGACACCG 436
DB |||||
QY 286 CTGGAGATGTTTCTCAAGCCGCTGTGATCTTGCCCTGCAACACACCTGTGCGCAAG 345
DB |||||
QY 437 TGTGCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACGCGGCTGCTCAGTG 496
DB |||||
QY 346 TGTGCAACGACGCTTCTCCAGGCTTAACTCTCTGTGGCAATCCCGGGCTCCCAACG 405
DB |||||
QY 497 TCCATGTCTGGAGGCTGTTTCCGTTGCCCTCTGTCGCCCATGAAAGTATGATGACACCG 556
DB |||||
QY 406 GTGCTCTCAGGAGGACGTTTCCGATGCCCACTTGTAGGACGAGGTTGCTCTGACAGG 465
DB |||||
QY 557 CACGGGGTGTAGGGCTTCAGAGAACCTGTGTTGGGAAACATCATTTGACATCTCAAG 616
DB |||||
QY 466 CATGTGTCTATGGCTTCAGCGGAACCTGTGTAGTGGAGAACATCATTTGACATCTCAAG 525
DB |||||
QY 617 CAGGAGTCTCCAG---TCGGCCCTTCAGAAAGCAGCCACCCATGTGCAAGNAC 673
DB |||||
QY 526 CAGGAGTCTTCCAGGCTGCAACGCTGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 585
DB |||||
QY 674 GAAGACGAGAGATCAACATCTACTGTCTCAGGTGTGAGGCTGCTACTGCTCTTGTGC 733
DB |||||
QY 586 GAGGACGAGAGATCAACATCTACTGTCTGAGCTGCGAGGTCGCCACCTGCTCTCTCTC 645
DB |||||
QY 734 AAGGTGTTTGGGGCTCACCAGGCTGTGAGGTTGCCCTTTGCAAGCATCTTCCAAAG 793
DB |||||
QY 646 AAGGTGTTTGGGGCTCACCAGGCTGTGAGGTTGCCCTTTGCAAGCATCTTCCAAAG 705
DB |||||
QY 794 CAGAAAGCTGAGCTGAGTAACTGCACTCTCCATGCTGGTGGCGGGGAAACGACGAGTGCA 853
DB |||||
QY 706 CAGAAAGCTGAGCTGAGTAACTGCACTCTCCATGCTGGTGGCGGGGAAACGACGAGTGCA 765
DB |||||
QY 854 ACGATCATCTCAGCTGGAGGACTGTGTCAGAGTGACCAAGGAGAAATAGCCACAGGTG 913
DB |||||
QY 766 GCAGTGATCACCCAGATGGAGGAGGTGTCAGACCATTTAGGACAAACAGCGCGACAG 825
DB |||||
QY 914 AAGGAGGAGCTGAGTCAGAGGTTTGCACCTCTAGCCCATCTGATGAGAGAGAGAGAG 973
DB |||||
QY 826 AAGCAACTTTAAACAGAGGTTTGCAGACCTTGTGCGGCTTTTGGAGGAGCGCAAGGGC 885
DB |||||
QY 974 GAGCTGCTCAGCGGATCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1033
DB |||||
QY 886 GAATGCTTCAGCACTGCGCCCGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 945
DB |||||
QY 1034 ATCTCTCAGTACGAGGAGCAGCTGGAAAGTCCACCAAGCTTTGTGAGACCCGCTTCCAG 1093
DB |||||
QY 946 ATCCGCGCAGTACGAGACCACTTGGAGGCTCTCTCAAGCTGTGAGTCCGCCATCCAG 1005
DB |||||
QY 1094 TCCCTGGATGAGCCCGGAGGAGGAGTACCTTCTCTCAAGTGTGCAAGCAGCTCATCAAGAG 1153
DB |||||
QY 1006 TCCATGGAGGAGCGCAGATGGCTCTCTTACCTTCCAGCAGGAGGAGGAGGAGGAGGAGGAG 1065
DB |||||
```

```
RESULT 17
US-10-775-627-1
; Sequence 1, Application US/10775627
; Publication No. US20040142446A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028USD1
; CURRENT APPLICATION NUMBER: US/10/775,627
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1296)
US-10-775-627-1
```

```
Query Match      30.3%; Score 484.6; DB 19; Length 1431;
Best Local Similarity 69.2%; Pred. No. 1.2e-142;
Matches 677; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

QY 317 CTGATTCCTGATGGAAACCTATGGAGAACCTGGAGAACGACGCTGATGCCCCATCTGC 376
DB |||||
QY 226 CTGCTAGGGGATGGCAACATGACAACTTGGAGAACGCTCATTTGCCCCATCTGC 285
DB |||||
QY 377 CTGGAGATGTTTACCAAGCCTGTGTCATCTCTGCTCCCTGCGCAACAACTCTGCGGAAG 436
DB |||||
QY 286 CTGGAGATGTTTCTCAAGCCGCTGTGATCTTGCCCTGCAACACACCTGTGCGCAAG 345
DB |||||
QY 437 TGTGCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACGCGGCTGCTCAGTG 496
DB |||||
QY 346 TGTGCAACGACGCTTCTCCAGGCTTAACTCTCTGTGGCAATCCCGGGCTCCCAACG 405
DB |||||
QY 497 TCCATGTCTGGAGGCTGTTTCCGTTGCCCTCTGTCGCCCATGAAAGTATGATGACACCG 556
DB |||||
QY 406 GTGCTCTCAGGAGGACGTTTCCGATGCCCACTTGTAGGACGAGGTTGCTCTGACAGG 465
DB |||||
QY 557 CACGGGGTGTAGGGCTTCAGAGAACCTGTGTTGGGAAACATCATTTGACATCTCAAG 616
DB |||||
QY 466 CATGTGTCTATGGCTTCAGCGGAACCTGTGTAGTGGAGAACATCATTTGACATCTCAAG 525
DB |||||
QY 617 CAGGAGTCTCCAG---TCGGCCCTTCAGAAAGCAGCCACCCATGTGCAAGNAC 673
DB |||||
QY 526 CAGGAGTCTTCCAGGCTGCAACGCTGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 585
DB |||||
QY 674 GAAGACGAGAGATCAACATCTACTGTCTCAGGTGTGAGGCTGCTACTGCTCTTGTGC 733
DB |||||
QY 586 GAGGACGAGAGATCAACATCTACTGTCTGAGCTGCGAGGTCGCCACCTGCTCTCTCTC 645
DB |||||
```

```
QY 734 AAGTGTGTTGGGGCTACCAAGGCGCTGTGAGGTGGCCCTTTGCAAAAGCATCTTCCAAAGGA 793
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
646 AAGTGTGTTGGGGCTACCAAGGCGCTGTGAGGTGGCCCTTTGCAAAAGCATCTTCCAAAGGC 705
QY 794 CAGAAGACTGAGCTGAGTAACTGCATCTCCATGCTGTGTGGGGGACGACCGAGTGCAG 853
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
706 CAGAAGAGTGAAGCTGAGCGATGCGCATGCTGTGTGGGGGCAATGACCGTGTGCAG 765
QY 854 ACATCATCTCTCAGCTGGAGGAGCTCGTGCAGAGTGCACCAAGGAGAAATAGCCACCAAGGTG 913
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
766 GCAGTGATCACCAAGTGGAGGAGTGTGCAGACCAATTGAGAGACACAGCCGACAGACAG 825
QY 914 AAGAGAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCTCGATGAGAAAGAGAGC 973
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
826 AAGCAACTGTAAACCAAGAGGTTTCGAGACCCCTGTGCGCGTGTGAGGAGCGCAAGGGC 885
QY 974 GAGCTCTGACGGGATCACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1033
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
886 GAACCTGCTTCAAGCACTGGCGCGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 945
QY 1034 ATCCTTCAGTACAGGAGCAGCTGGGAAAGTCCACCAAGCTTGTGGAGCCGCGCATCCAG 1093
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
946 ATCGCCAGTACGAGACCACTTGGAGGGCTCTCAAAGCTGTGTGAGTCCGCGCATCCAG 1005
QY 1094 TCCTTGATAGCCCGGAGGGGTACTTCTCTCAAGTGCCCAAGCAGGCTCATCAAGAGC 1153
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1006 TCCATGAGGAGCGCGAGATGGCTCTCTACCTCCAGCAGGCAAGGAGCTGATCAACAAAG 1065
QY 1154 ATTGTAGAGCTTCCAGGCTCCAGCTGGGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1213
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1066 GTCGGGGCAATGTCGAAGGTGGAGCTGGCAGGAGCGCGGAGGAGGAGGAGGAGGAGGAGG 1125
QY 1214 GACTACTTTACTCTGGAACATAGACAGAGGCGCTTGAAGGCGCATTTGAGCTTTGGG 1273
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1126 GAGCAATCTCTGAGCTGGAGCAGCTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1185
QY 1274 ACAGGTAAAGAGTGTGATG 1292
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1186 CCGGGCGCGCTGGGATG 1204
```

RESULT 18

```
US-09-890-688-57
; Sequence 57, Application US/09890688
; Publication No. US20030144475A1
; GENERAL INFORMATION:
; APPLICANT: Seishi KATO
; APPLICANT: Chikashi EGUCHI
; APPLICANT: Minoru SAEKI
; TITLE OF INVENTION: Human Proteins and cDNAs thereof
; FILE REFERENCE: 2001-1102A/WMC/00653
; CURRENT APPLICATION NUMBER: US/09/890,688
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: JP 11-346863
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: JP 11-34684
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: JP 2000-31062
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: JP 2000-34091
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: JP 2000-34090
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: JP 2000-35829
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-35899
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-71161
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: JP 2000-160851
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 57
; LENGTH: 1913
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (303)..(1379)
US-09-890-688-57
```

```
Query Match 30.2%; Score 481.8; DB 10; Length 1913;
Best Local Similarity 69.4%; Pred. No. 1.1e-141;
Matches 670; Conservative 0; Mismatches 292; Indels 3; Gaps 1;

QY 317 CTGATTCCTGATGGAACCGTATGGAGAAACCTGGAGAAAGCAGCTGATCTGCCCATCTTGC 376
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
330 CTGCTAGGGGATGCAACAGCATGGACAACCTGGAGAAAGCAGCTCATCTGCCCATCTGC 389
QY 377 CTGGAGATGTTTACCAAGCCTGTGFTCATCTTCGCCCTGCAACACAACTCTTGCAGGAAG 436
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
390 CTGGAGATGTTCTCCAAACAGTGGTGATCTCTGCCCTGCAACACAACTGTGCCGCAA 449
QY 437 TGTGCCAACGACATCTTCCAGGCTGCGAATCCCTACTGGACCAACCGCGGTGGCTCAGTG 496
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
450 TGTGCCAACGACGCTCTTCCAGGCTCGAATCTCTTATGGAAGTCCCGGGCTCCACCACT 509
QY 497 TCCATCTCTGGAGGTGCTTTCCGTTGCCCTCGTGGCGCATGAAGTGATCATGGACCGG 556
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
510 GTGTCTTCAGGAGGCGGTTTCCGCTGCCCATCGTGGAGCATGAGGTTGTCTGGACAGA 569
QY 557 CACGGGGTGTACGGCTGCGAGAGAACCTGTGTTGGTGGAAACATCATTCATCTTCAAG 616
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
570 CACGGTGTCTACGGCTGCGAGGAAACCTGTGTAGTGGAGAAATTATCGACATTTACNAAG 629
QY 617 CAGGAGTGTCTCAG ---TCGGCCCTGCGAAGAGCAGCCACCCGATGTGCAGGAACAC 673
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
630 CAGGAGTGTATCAGGCGCGTGCATCTCAAGGCTGAGCAGCACCTCATGTGCGAGGAGCAT 689
QY 674 GAAGACGAGAAGATCAACATCTACTGTCTCAGTGTGAGGTGCTTACTTGTCTTGTGC 733
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
690 GAAGAAGAGAGATCAATATTTACTGCTGAGCTGTGAGGTGCCACCTGCTCTCTCTGC 749
QY 734 AAGGTGTTTGGGGCTCACCAGGCTGTGAGGTTGCCCTTTGCAAAAGCATCTTCCAAAGGA 793
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
750 AAGGTCTTCGGTGCACCAAGGACTGTGAGGTGGGCCCTGCCCCACCATTTACAAACGC 809
QY 794 CAGAGACTGAGCTGAGTAACTCTCCATCTGCTGTGGCGGGGAAACGACGAGTGCAG 853
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
810 CAGAAGAGTGAAGCTCAGCGATGCGCATGCTGTGTGGAGGAGAAAGTGCAGCGCGTGC 869
QY 854 ACGATCATCTCTCAGCTGAGGAGCTGCTGAGAGTGAACCAAGGAGAAATAGCCACCAAGGTG 913
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
870 GCAGTGATCACACAGATGGAGGAGGTGTGCCAGACTATCGAGGACATATAGCCGAGGCAG 929
QY 914 AAGGAGGAGCTGAGTCAAGATTTGACACCTCTTACGCCATCTCTGATGAGAAAGAGC 973
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
930 AAGCAGTTCCTTAAACCAAGAGGTTTGAGAGCTGTGCGCAGTGTCTGGAGGAGCGCAAGG 989
QY 974 GAGCTCTCAGCGGATCACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1033
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
990 GAGCTGCTCAGCGCGCTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1049
QY 1034 ATCTCTCAGTACAGGAGCAGCTGGAAAGTCCACCAAGTGTGTGGAGACCGCATCCAG 1093
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1050 ATCCGTGAGTATGGCGACCACTGAGGGCTCTCTTAAGCTGTGGAGTCTGCCATCCAG 1109
QY 1094 TCCCTGGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGGCCAGCAGCTCATCAAGAGC 1153
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1110 TCCATGGAAGAGCCCAAAATGGCGCTGTATCTCCAGCAGGCGCAAGGAGCTGATCAATAAG 1169
QY 1154 ATTGTAGAGGCTTCAAGGGGCTGCCAGCTGGGGAAGACAGAGCAAGGCTTTGAGAAACATG 1213
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1170 GTCGGGGCCATGTGGAAGTGGAGCTGGCAGGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1229
```


Db	328	CAGGAGTCATCCAGGCGCTGCATCCAAAGCTGAGCAGCACCTCATGTGCGAGGAGCAT	387
Qy	674	GAAGACGAGAGATCAACATCTACTGTCTCACGTGTGAGGTGCTACTTGTCTCTTGTGC	733
Db	388	GAAGAAGAGAATCAATATTACTGCCTGAGCTGTGAGGTGCCACCTCTCTCTCTGC	447
Qy	734	AAGTGTTTGGGGCTACCAAGGCTGTGAGGTGCCCTTTGCAAAAGCATCTTCCAAAGGA	793
Db	448	AAGGTCTTTCGGTGGCCCAAGGACTGTGAGGTGGCCCCACTGGCCACCAATTACAAAGC	507
Qy	794	CAGAAGACTGAGCTGAGTAATCTCATCTGCTGTGGCGGGACGACCGAGTGCAG	853
Db	508	CAGAAGAGTGAGCTCAGCGATGGCATGCCATGCTGTGGTGAGGCAATGACCCGCTGCAA	567
Qy	854	ACGATCATCTCTCAGCTGGAGGACTCGTGCAGAGTGACCAAGGAGAAATAGCCACCAAGTG	913
Db	568	GCAGTGATCACACAGATGGAGGAGGTGTGCCAGACTATCGAGGACATAGCCCGAGGCAG	627
Qy	914	AAGGAGAGCTGAGTCAGAAAGTTTGACACCCCTCTACGCCATCCTGGATGAGAAAGAGC	973
Db	628	AAGCAGTTGTTAAACCAAGAGGTTTGACAGCCTGTGCGCAGTGTGGAGGAGCGCAAGGT	687
Qy	974	GAGTGTCTGACGGGATCACGACGAGGACGAGGAGGAGCTGGGCTTCATCGAGGCTCTG	1033
Db	688	GAGTGTCTGACGGGCTGGCCCGGAGCAAGAGGAGAACTGCAGCGCGTCCGCGCCTC	747
Qy	1034	ATCCTCCAGTACAGGGAGCAGCTGGAAAGTCCACCAAGCTTGTGGAGACCGCATCCAG	1093
Db	748	ATCGTCAGTATGGCGACCACTGGAGGCTCTCTTAAGCTGTGGAGTCTGCCATCCAG	807
Qy	1094	TCCCTGATGAGCCCGGAGGGGCTACCTTCTCTCAAGTGCCCAAGCAGCTCATCAAGA	1151
Db	808	TCCATGGAGAGGCCCAAAATGGCGTGTATCTCCAGCAGGCCCAAGGAGCTGATCAATA	865

Search completed: June 15, 2005, 14:37:51
 Job time : 921 secs